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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Buthoria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 630)
Barchan, D. and Fuchs, S.
RECOMBINARY FRAGMENTS OF THE HUMAN ACETYLCHOLINE RECEPTOR AND THEIR USE FOR TREATMENT OF MASTHENIA GRAVIS
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A83283 630 bp Sequence 3 from Patent WO9850544.
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
ACCESSION
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A83283
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(without alignments)
5884.072 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                         2054640 seqs, 14551402878 residues
                                                                                                                                                                                                                                                                 tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                               - nucleic search, using sw model
                                                                                          January 14, 2003, 14:17:52
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AR037435 Sequence U64431 Human nicot V06418 H.saptens m U65432 Human nicot M37981 Human alpha BC00296 Homo sapi BC000513 Homo sapi BC001642 Homo sapi AJ750360 Gallus ga L31621 Rattus norv X03440 Rat mRNA fo

Homo sapien

Y16281

HSNACHR3A

1512 1908 1910 3020 3029

2046 1590 2277 2664

AR173185 HSNACHRA3

BC011490 Mus muscu AF325346 Mus muscu AF472588 Mus muscu AF472588 Mus muscu AF459029 Mus muscu AF225912 Mus muscu

RATNARA RNACHRAR EEU17016 BC011490 AF325346

99

Y08421 H.sapiens m J62433 Human nicot M86383 Homo sapien

HSNACHRA4 HSU62433 HUMA3NARSI

AF459029 AF225912 PAT 21-JAN-2000

linear

DNA

Pred. No. is the number of results predicted by chance to have a

ALIGNMENTS

X03986 Mouse mRNA M17640 Mus musculu X74832 R.norvegicu AJ250359 Gallus ga J00963 Ray (T.cali

S77094 nicotinic a M64695 Synthetic h X02509 B.Taurus mR AB021708 Canis fam

S77094 SYNHUMACRS

A83283 BC006314 HSACHRA

B

Length

BTACHRA1 AB021708 MMACHRAM MUSACHRAB

RNACRA1 GGA250359 FSCACHRA

XLACHRA1 KLACHRA

1815 2045

A83283 Sequence 3 BC006314 Homo sap1 Y00762 Human mRNA

Description

SUMMARIES

AR106255 Sequence M2593 T.marmorata X07067 Xenopus mRN X17244 Xenopus mRN U70438 Danio rerio X57032 B.taurus mR AR055253 Sequence AR071401 Sequence AR071401 Sequence X5359 H.sapiens H AF385584 Homo sapi

FEATURES

ORIGIN

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Web site:
    http://www.nisc.nih.gov/
Contact:
    nisc_mgc@hhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"Similar to cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)" protein-id="AAH06114.1" /db.xref="GI:15624429" /translation="MEPWPLLLFSLCSAGLVLGSEHETRLVAKLFKDYSSVVRPVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRQVVEVTVGLOLIQLINVDEVNQIVTINVRLKQQWVDXNLKWNPDDYGGVKKIHIPS
EKIMRPDLVLXNNAGDFAIVKFTKVLLQYTGHIFWPPAIFKSYCEIIVHFPFFDEQ
EKSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKESRGWKHSVTXSCCPDTPY
LDITYFFVWRLPLPYLVVVIIPCLLFSFLTGLVFYLPTDSGGCGCHDCCC"
432 c 365 g 377 t
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                                                                    Submitted (09-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                        Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland;
Web site:
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/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
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Pred. No. 3.9e-136;
0; Mismatches 1;
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/db_xref="taxon:9606"
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                                                                                                                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                         Tissue Procurement: ATCC
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Catarrhini; Hominidae; Homo.
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Homo sapiens, Similar to cholinergic receptor, nicotinic, alpha
polypeptide 1 (muscle), clone MGC:12708 IMAGE:4124038, mRNA,
                                                                                                                                   ACETYLCHOLINE RECEPTOR
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100.0%; Pred. No. 1.5e-136;
ive 0; Mismatches 0;
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                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Extracellular DoMAIN
ALPHA-SUBUNIT"
                                                                                                                                                                           ¥
WO 9850544-A 3 12-NOV-1998;
DORA (IL); FUCHS SARA (IL)
Location/Qualifiers
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Mammalia; Eutheria; Primates;
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/ DOCUMENT CAREAL CARE BY 31.1"

/ ABD. XIEFF = "G1: 28309"

/ ABD. XIEFF = "G1: 28309"

/ ABD. XIEFF = "G1: 28709"

/ ABD. XIEFF = "G1: 28709"

/ LIABS = "BEWFLLILE'SLCSAGLVLGSEHETRLVARLERDYSSVVRPVED

RROWEDVILVINNABODE SATWETRYLLOYTORITHTWPP PATENTSYCELITYHEPEDED

NCSMKLGTWITYDGSVVAINUESDOPDI.SNPMESGEWVINGSRGWKRSVTSCCPOTPY

LDITYHFVWORLPLYFIVNVIIPCLLE'SFLTGLVFYLPTDSGEKMTLSISVLLSLTVF

LIATVELIPSTSSAVPLIGKYMLFTWYFVIASITITYJVINTHRSPSTHYWBINWYRK

VIEDVIENINKEPSTRKRPSRERODEKIFTEDIDISISISSRGFGFPPRAGFHSFLIKHEBS

KSAIEGIKYIAFTRINGSPRADESORKIFTEDIDISISISSRCFGFPPRAGFHSFLIKHEBS

KSAIEGIKYIAFTRINGSPRADESORKIFTEDIDISISSRCFGFPPRAGFHSFLIKHEBS

KSAIEGIKYIAFTRINGSPRADESORVANAAAEWKYVAMVMDHILLGVPMLVCIIGTLAVFAGFL
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Submitted (03-FPB-1988)
Submitted (03-FPB-1988)
Schoepfer, R., Luther, M. and Lindstrom, J.
The human medulloblastoma cell line TE671 expresses a muscle-like acetylcholine receptor. Cloning of the alpha-subunit cDNA BBII2T90
3338555
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 1667)
Schoepfer, R.
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                                                                                                                                                                                                 A 167 bp mRNA linear PRI 23-
mRNA for muscle acetylcholine receptor alpha-subunit.
            GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCT
                                                                        489 CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAG
                                                                                                                                                                                 421 AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGCCTCTGTCGTGGCCATCAACCCG
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/db_xef="taxon:9606"
/clone="prE1.1"
/cell_line="medulloblastoma TE761"
/clone_lib="TFE"
/9. .1422
/note="precursor (AA -20 to 437)"
                                                                                                                                                                                                                                                                                                                                                                       ATCACCTACCACTTCGTCATGCAGCGCCTG 630
                                                                                                                                                                                                                                                                                                                                                                                     acetylcholine receptor alpha.
Homo sapiens,
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/organism="Homo
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1676 bp mRNA linear PRI 26-SEP-1995 nicotinic acetylcholine receptor alpha subunit|AChR alpha subunit |human, thymic carcinoma, myasthenia gravis-associated thymoma patient 1494/88, mRNA Partial, 1676 nf].
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Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1676)
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            49...108
109..1419
Pyroduct="mature alpha-chain (AA : 529..531
/note="pot. N-glycosylation site"
A 465 c 371 g 412 t
                                                                                                                                                                       Score 628.4; DB 9;
Pred. No. 3.9e-136;
); Mismatches 1;
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11 Similarity 99.8%;
629; Conservative
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/translation-"MSEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLIQLINV
DEVNOIVTHVRLKQOWLDYNLKWNBDDYGGVKTHIPSEK TWRPDLVLXNNADGDFA
DIVKFTKVLLQVTGTTTTPTPALFE TEKSYCEI TVTHFPEDGONCSMKLGTWTYDGSVVAIN
PESDQPDLSNPMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHFVIQRL
                                                                                                                                                                                                                            ; 645 bp DNA linear SYN 27-APR-1993
human acetylcholine receptor alpha subunit gene, complete
                                                                                                                                                                                                                                                                                                                                                       artificial sequences.

1 (bases 1 to 645)
Talib,S., Leiby,K., Wright,K. and Okarma,T.B.
Cloning and expression in Escherichia coli of a synthetic gene encoding the extracellular domain of the human muscle acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTCAGAAAAGATCTGGCGCCAGACCTTGTTCTCTATAAQAAGAGGAGATGGAGCTTT 308
                                                           9 TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGGGG
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        541 TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC
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/product="acetylcholine receptor alpha subunit"
/protein.id="ak473020.1"
/db_xref="G1:208506"
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/gene="acetylcholine receptor alpha subunit"
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Pred. No. 4.8e-135;
); Mismatches 4;
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/db_xref="taxon:32630"
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synthetic construct
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ilarity 99.4%;
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Gattenlohner, S., Brabletz, T., Schultz, A., Marx, A.,
Muller-Hermelink, H.K. and Kirchner, T.
Cloning of a cDNA coding for the acetylcholine receptor
alpha-subunit from a thymoma associated with myasthenia [correction
of myastenia] gravis
Thymus 23 (2), 103-113 (1994)
7725386
                                                                                                                                                                                                                                                                                                                                                                                   Translation-"MEEPPLLIFSICSAGIVLGSEHETRLYARLEKDYSSVYRPVED
HRQVVEVYTVGLOLINVDEVNQIVTINVRLKQQWVDYNLKWNPDDYGGVKKIHIPS
EKTWPPDLIVYINNADGDFAIVETRVLLQYTGHTTWPPPAIRENSYCEITTYHPPFDEQ
NCSMKLGTWYTDGSVVAINPESDQPDLSNPRESGEWYLESGGWKHSYTSCCPDTPY
LDITYHFVMQRLPLYFIVNVIIPCLLFSFLTGLVFYLPTDSGEKWTLSISVLLSLTVF
LILIVELIPSTSSAVPLIGKYMLFFNFVVIASTITTYJVINHHRSPSTHYMNWVR
KIDITINNIMFFSTHXRPSRENGDKIFTEDIDISDISGROPPMGFHSPLIKHFEY
KSAIEGIKYIAFFHYNVAINAAAEWKYVAMVMDHILLGVFMLVCIIGTLAVFAGRL
                                                                                                                                                                                                                                                         subunit | AChR
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                                                                                                                                       GenBank staff at the National Library of Medicine created thi
entry [NCBI glbbsq 164456] from the original journal article.
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.db_xref="taxon:9606"
.1.676
/gene="nicotinic acetylcholine receptor alpha
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Pred. No. 3.9e-136;
); Mismatches 1;
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/db_xref="G1:4261947"
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B.Taurus mRNA for acetylcholine receptor alpha (AChR) precursor.
X02509.1 GI:49
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1 (bases 1 to 3618)
Noda,M., Furutani,Y., Takahashi,H., Toyosato,M., Tanabe,T., Shimizu,H., Kikyotani,S., Kayano,T., Hirose,T., Inayama,S. and
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Evans, P.
Direct Submission

Submitted (07-SEP-1992)
Data kindly reviewed (04-MAR-1986)
Location/Qualifiers
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/protein_id="CAA26345.1"
/db_xref="G1:50"
                                                                                                                                                                                                                                            /organism-"Bos taurus"
/db_xref-"taxon:9913"
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AB021708
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Pred. No. 3.5e-121;
0; Mismatches 41;
/product="AChR prepeptide"
2129. .2147
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Best Local Similarity 93.5%;
Matches 589; Conservative (
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ROD 12-SEP-1993

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/translation="MELSTVLLLDLCSAGLVLGSEHETRLVAKLFEDYSSVVRPVED
/translation="MELSTVLLLLGLCSAGLVLGSEHETRLVAKLFEDYSSVVRPVED
/translation="MELSTVLLLLDYTCHITYTPPAIFKSYCEITVTHPPFDED
/translation="MELSTVLLLDYTCHITYTPPAIFKSYCEITVTHPPFDED
/translation="MELSTVLLLSTCHTTPPAIFKSYCEITVTHPPFDED
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/translation="MELSTVLTSTCHTPPEDSGEWITSSCTTTPPY
/translation="MELSTVLTSTTP"
/
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoberg, K.E., Mudd, J., Shah, V. and Merlie, J.P.
Nucleotide sequence of the mouse muscle nicotinic acetylcholine receptor alpha subunit
Nucleic Acids Res. 14 (12), 5111 (1986)
86259081
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                                                                                                                                                                                                                                                                                                                                                                                       RAM 1769 bp mRNA linear ROD 12-S:
mRNA for muscle nicotinic acetylcholine receptor alpha
                                                 1 TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG
                           GAAAGCGACCAGACCTGAGCAACTTCATGGAGAGGGGGGAGTGGGTGATCAAGGAG
                                                                                                                        TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC
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Pred. No. 3e-112;
0; Mismatches 65; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Data kindly reviewed (15-AUG-1986) by J. Merlie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                X03986.1 GI:49848 acetylcholine receptor alpha; membrane protein. Mus musculus.
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/db_xref="taxon:10090"
                                                                                                                                                                                                                 ATCACCTACCACTTCGTCATGCAGCGCCTG 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="nicotinic acetylcholine recepter alpha-subunit"
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/db_xref="01:4889714"
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LDITYFFVNNADGPAIVKTPSFLGLFSFLGLYFYLPTSGEKMTLSISVLSITVF
LLAIVELIPSTSSAPPLIGKKMLFTWNFVIASIIITVIVNTHRSPSTHVWEDWVRK
VFIDTIPNIMFFSTRAKRPSREKQDKKIFFEDIDISDISGKROFPPROMCHSPLIKHPEV
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IELNLQG"
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                        Yoshioka,T., Uzuka,Y., Tanabe,S., Sarashina,T. and Ishiguro,N. Molecular cloning of the canine nicotinic acetylcholine receptor alpha-subunit gene and development of the ELISA method to diagnose
                                                                                                                                                                                                               Direct Submission
Submitted (22-DEC-1998) Tasuku Yoshioka, Obihiro University of
Agriculture and Veterinary Medicine, Laboratory of Veterinary
Internal Medicine: Inadacho Nisi2-11, Obihiro, Hokkaido 080-0834,
Japan (E-mail:s05039@st.obihiro.ac.jp, Tel:81-155-49-5371,
Fax:81-155-49-5374)
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20092256
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Pred. No. 1.8e-120;
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Canis familiaris"
/db_xref="taxon:9615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="nachr alpha-subunit"
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5. .1379
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    (sites)
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CSKKLGWYWTDGSVVAINPESDQPDLSNFWESGEWYIKEARGWKHWYTGSCPTTPY
LDTTYFFWQRLPLFTNNVIIPCLLFSFLTSLVFYLPTDSGEKWTLSISVLLSTTVF
LLVIYELIPSTSSAPVPLIGKYMLFTWFVIASIIITVTVINTHRRSPSTHINPEWVR
VFIDTIPNIMFFSTWKRPSRDKQEKRIFTEDIDISDISGKPGPPPMGFHSPLIKHPEV
STSIEGVKYIAETMKSDQESNNAABEWKYVAMYMDHILLGVFMLVCLIGTLAVFAGRL
IELHQOG"
498 c 436 g 478 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCT
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                                                                                                                                                           Length 1860;
                                                                                                                                                                                       Indels
                                                                                                                                                           Score 526; DB 10;
Pred. No. 3e-112;
0; Mismatches 65;
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acetylcholine receptor alpha.
Rattus norvegicus.
Rattus norvegicus.
Bukaryota; Metazoa; Chordata; Ci
                                                                                                                                                           83.58;
89.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.norvegicus mRNA for X74832
                                                                                                                                                                         Best Local Similarity 89.7
Matches 565; Conservative
                                                                                                              448
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HREIVQYTVGLQLIQLINVDEVNQIVTTNVRLKQQWVDYNLKWMPDDYGGVKKIHIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROD 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-MAY-1997) Psychiatry, UCLA, 760 Westwood Plaza, Los Angeles, CA 90095-1759, USA sequence update on May 8, 1997 this sequence version replaced gi:191601.

Location/Qualifiers 1. 1860
//Organism="Mus musculus"
//db_aref="hasha.ton:10090"
//clone="pbMA407"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACHRAB 1860 bp mRNA linear ROD 09-MAY-19 musculus acetylcholine receptor alpha-subunit mRNA, complete
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                                                                                                            GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCT 360
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Boulter, J. Luyten, Mountain, Sciurognathi; Muridae; Murinae;
Boulter, J., Luyten, W., Evans, K., Mason, P., Ballivet, M., Goldn Stengelln, S., Martin, G., Heinemann, S. and Patrick, J.
Isolation of a clone coding for the alpha-subunit of a mouse acetylcholine receptor
J. Neurosci. 5 (9), 2545-2552 (1985)
CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTTGATGAACAG
                                                                                                                                                                                                                                    AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCCG
                                                                                                                                                                                                                                                                  AACTGCAGCATGAAGCTGGGCACCTGGACCTATGACGGCTCTGTGGTGGCCATTAACCCG
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                                               CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
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/protein_id="AAB53942.1"
/db_xref="GI:2073544"
                                                                                                                                                                                                                                                                                                                                                                                                                     ATCACCTACCACTTCGTCATGCAGCGCCTG 630
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M17640.1 GI:2073542
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Direct Submission
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JOURNAL
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420

360

480

644

600

1849 bp mRNA linear ROD 14-SEP-1999 acetylcholine receptor alpha-subunit. Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 1849)
Witzemann,V., Stein,E., Barg,B., Konno,T., Koenen,M., Kues,W.,

26-OCT-1999

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/translation="MELCRVILLIFSAAGPALCYEHETRLVDDLFREYSKVVRPVENH
RDAVVVTVGLQLIQLINVDEVNQIVTTNVRLKQQWTDINLKWNPDDYGGVKQIRIPSD
DIWRPDLVLYNNADGDFAIVKYTKVLLEHTGKITWTPPAIFKSYCEIIVTYFPFDQON
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DITYHFLMORLPLYFIVNVIIPCLLESFLTGFWYLYLPTDSGERMTLSISVLLSCHVFL
LEVIVELIPSTSSAVPLIGKYMLFTWFVIASIIITVIVINTHHRSPSTHTMPPWYRKI
FIDT TPNIMFFSTMRKPSRNKTNFKTFAEDLDISETSGROGFVPVNFYSPLTRNPDVR
NAIEGIKYIAETMKSDQESSNAADEWKFVAMVLDHLLLUIFMLVCIIGTLAVFAGRLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves: Neognathae; Galliformes; Phasianinae; Gallus.

1 (bases 1 to 1393)
Nef,P., Oneyser,C., Alliod,C., Couturier,S. and Ballivet,M. Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptors
EMBO J. 7 (3), 595-601 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGA250359 1393 bp mRNA linear VRT 26-OCT-19
Gallus gallus mRNA for nicotinic acetylcholine receptor, alpha-1
subunit (nachral gene).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-1 subunit; nachral gene; nicotinic acetylcholine receptor
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Ballivet, M.
Direct Submission
Submitted (25-OCT-1999) Ballivet M., Biochemistry, University
Geneva, 30 qual Ennest Ansermet, 1211 Geneva 4, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="nicotinic acetylcholine receptor, alpha-1
                                                                                                                                                              GCCCGGGGCTGGAAGCACTGGGTGTTTTACTCCTGCTGCCCCAACACCCCTTATCTGGAC
                                                                             542 AACTGCAGCATGAAGCTGGGCACTTGGACCTATGACGGCTCTGTGGTGGCCATCAATCCG
                                                                                                                                541 TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC
                                AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="CAB59624.1"
/db_xref="GI:6136924"
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/db_xref="taxon:9031"
/tissue_type="muscle"
                                                                                                                                                                                                                                                                                                                                       601 ATCACCTACCACTTCGTCATGCAGCGCCTG 630
                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="neonate"
/country="Switzerland"
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/gene="nachral"
/codon_start=1
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7. .1377
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/gene="nachral"
64. .1374
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Gallus gallus
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GGA250359
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TITLE
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AUTHORS
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/product="acetylcholine receptor alpha-subunit"
/product="acetylcholine receptor alpha-subunit"
/do_xref="g1:39882"
/d
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Criado,M., Hofmann,M. and Sakmann,B.
Primary structure and functional expression of the alpha-, beta-,
gamma-, delta- and epsilon-subunits of the acetylcholine receptor
                                                                                                                                                                                                                                 Direct Submission
Submitted (10-AUG-1993) V. Witzemann, Max-Planck-Institut, fuer
Medizinische Forschung, Abt. Zellphysiologie, Jahnstrasse 29, D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCCACTTTCCCTTTGATGAACAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 1.7e-111;
); Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hind leg
                                                                                        Eur. J. Biochem. 194 (2), 437-448 (1990)
91099317
                                                                                                                                                                                                                                                                                                                                                               1. .1849
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10116"
/clone="racr-alpha"
/tissue_type="denervated hi
/clone_lib="lambda gt10"
/dev_stage="adult"
62. .1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457
                                                                                                                                                                                                                                                                                                            69120 Heidelberg, FRG
Location/Qualifiers
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Witzemann, V.
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122. .1432
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mat_peptide
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ORIGIN
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PUBMED
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2 (bases 1 to 2045)
Noda,M., Takahashi,H., Tanabe,T., Toyosato,M., Furutani,Y.,
Hirose,T., Asai,M., Inayama,S., Miyata,T. and Numa,S.
Primary structure of alpha-subunit precursor of Torpedo californica
acetylcholine receptor deduced from cDNA sequence
Nature 299 (5886), 793-797 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The alpha subunit for the acetylcholine receptor consists of 461 amino acids including a 24 amino acid prepetide. This subunit is thought to contain the acetylcholine binding site and [1] suggests possible sites. Although the sequences ([1] versus [2], [4]) differ at > twenty sites, this probably reflects species variation, since all propose the same protein sequence with exception of the amino acid residue 42 (site 383). [2] argues that the single mRNA species for achr-alpha falls to cross-hybridize with the same mRNA from cat muscle. [4] proposes a model for the transmembrane organization of the alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                    Numa, 5., Noda, M., Takahashi, H., Tanabe, T., Toyosato, M., Furutani, Y. and Kikyotani, S.
Molecular structure of the nicotinic acetylcholine receptor Cold Spring Harb. Symp. Quant. Biol. 48 Pt 1, 57-69 (1983)
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RLPSDDVWLPDLVLYNNADGDFAIVHMTKLLLDYTGKIMWTPPAIFKSYCEIIVTHFP
FDQQNCTMKLGIWTYDGTKVSISPESDRPDLSTFMESGEWVMKDYRGWKHWVYYTCCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTVFLLVIVELIPSTSSAVPLIGKYMLFTMIFVISSIIITVVVINTHHRSPSTHTMPO
WVRKIFIDTIPNVMFFSTMKRASKEKQENKIFADDIDISDISGKQVTGEVIFQTPLIK
NPDVKSAIEGVKYIAEHMKSDEESSNAAEEWKYVAMVIDHILLCVFMLICIIGTVSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MILCSYWHVGLVLLEFSCCGLVLGSEHETRLVANLLENYNKVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTPYLDITYHFIMQRIPLYFVVNVIIPCLLFSFLTGLVFYLPTDSGEKMTLSISVLLS
                                                                                                                                                                                                                                                                Devillers-Thiery, A., Giraudat, J., Bentaboulet, M. and Changeux, J.P. Complete mRNA coding sequence of the acetylcholine binding alpha-subunit of Torpedo marmorata acetylcholine receptor: a model for the transmembrane organization of the polypeptide chain Proc. Natl. Acad. Sci. U.S.A. 80 (7), 2067-2071 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="c in [2],[4]; a in [1]"
187. 1572
/note="acetylcholine receptor alpha subunit"
alpha subunit of the acetylcholine receptor
Nucleic Acids Res. 10 (19), 5809-5822 (1982)
83064520

    2045
/organism="Torpedo californica"
/db_xref="taxon:7787"

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127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA96705.1"
/db_xref="G1:213218"
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846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in [2],[4];
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Torpedo californica
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (T.californica [1]; Torpedo marmorata [2],[4]) electric organ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA coding for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richards, B.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540
                                                                                                                                                                                                                                                                                                                                                                                     64 TACGAGCACGAGACGCGCCTGGTCGATGACCTGTTCCGGGAATACAGCAAGGTGGTGCGC 123
                                                                                                                                                                                                                                                                                                      180
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                      subunit, nicotinic acetylcholine
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                                                                                                                                                                                                                                                                                                                                                              121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GTGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAAATTCACATT
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                                                                                                                         Length 1393;
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Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
1 (bases 102 to 1191; 1207 to 1419)
Swmlkawa, K., Houghton, M., Smith, J.C., Bell, L., Richard
Barnard, E.A.
The molecular cloning and characterisation of cDNA cod
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Pred. No. 4e-89
0; Mismatches
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    /gene="nachral"
/product="alpha-1
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79.88;
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                                           receptor"
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PAT 14-FEB-2001
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Clark, B.R., Sharma, S.D. and Lerch, B.L.
MHC conjugates useful in ameliorating autoimmunity
Patent: US 6106840-A 1 22-AUG-2000;
                                                                                                                                         linear
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                                                                                                                                       AR106255 1350 bp
Sequence 1 from patent US 6106840.
AR106255
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     /organism="unknown"
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bases upstream of BglII site ([Nature 299, 793-797 (1982)]).
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                                                            [1]
                                                                                                                                                                                                                                 .753. .1/5.
'note="atg in [4]; gta in [1]"
                                   g in [1]"
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                                                                                                            g in [1]"
                                                                                                                                                                1697. 1698 ..., c in [1]"
/note="tta in [4]; ta in [1]"
[738. 1739
                                                                                                                                                                                                                                                                                                                                                                    ca in [1]"
                                                                                                                                                                                                               /note="g in [4]; ag in [1]"
[753. .1755
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1796
/note="c in [4]; a in [1]"
1808
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1620
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1697. .1698
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1824
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1850. .1851
/note="ag in [4]; ca in [1]
                                                            a in
         [2],[4];
                                                                                                            note="a in [2],[4];
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          'note="c
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2 (bases 1 to 1421)
Burden, S.J.
Direct Submission
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FDQONCTMKLGIWTYDGTKVSISPESDRPDLSTFWESGEWVWKDTRGWKHWYYYTCCP
DTPYLDITYHFIMQRIPLYFYVNVIIPCLLESETITVIFYLPPAIFSGEMTLSISVLCS
DTPYLDITYHFINGREPSAVPLIGKYMLFTMIFVISIIVTVVYINTHRSPSTHTMPQ
WVRK IFINTIPULMFSSTWKRASKEKOENK IFADDIDISDISGKQYTGEYIFOTPLIR
NPDVKSAIEGVKYIABHMKSDEESSNAAEEWKYVAMVIDHILLCVFWLIGIIGTVCVF
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/pictein_id="AAA96704.1"
/pictein_id="A216"
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PVEHHTHFVDITVGLQLIQLINVDEVNQIVETNVRLRQQWIDVRLRWNPADYGGIKKI
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Elasmobranchil; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1815) '
Devillers-Thiery,A., Giraudat,J., Bentaboulet,M., Klarsfeld,A. and
                                                                                                                                                                                                                                                                                                                                                       a model
                                                                                                                                                                                                                                                                                Torpediniformes; Torpedinoidel; Torpedinidae; Torpedo.

1 (bases 1 to 1815)

Devillers-Thiery,A., Giraudat,J., Bentaboulet,M. and Changeux,J.P.

Complete mRNA coding sequence of the acetylcholine binding
alpha-subunit of Torpedo marmorata acetylcholine receptor: a model

for the transmembrane organization of the polypeptide chain

Proc. Natl. Acad. Sci. U.S.A. 80 (7), 2067-2071 (1983)
                                                                                                                 FSCACHR 11-APR-:
T.marmorata acetylcholine receptor alpha-subunit mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular genetics of Torpedo marmorata acetylcholine receptor Adv. Exp. Med. Biol. 181, 17-29 (1984)
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0; Mismatches 172;
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T.marmorata electric organ, cDNA to mRNA.
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/db_xref="taxon:7788"
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Matches 454; Conservative
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SUNGSPULVLVINNADGDFAISKOPKILLEYTOKITWTPPATRSKCEIIUTYTPFDOQ
NCSKKFGTWTVGSLLVINERDRPDLSNFMASGEMMKDYRCWKHWYYTCCPDKPY
LDITYHFVLQRLDKIFYRIVNIIPCLLESFLTGLVFYLPFDSGERMTLSISVLLSLTVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulation of acetylcholine receptor transcript expression during development in Xenopus laevis
J. Cell Biol. 106 (2), 469-478 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                    361 CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAG 420
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X07067 Y00808
X07067.1 GI:64510
CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
1 (bases 1 to 1421)
BaldwinT.J., Yoshihara,C.M., Blackmer,K., Kintner,C.R.
Burden,S.J.
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Data kindly reviewed (31-Aug-1988) by Burden S.J.
Location/Qualifiers
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/organism="Xenopus laevis"
/db_xref="taxon:8355"
/tissuc_type="embryo"
/clone_lib="lambda gtl0, lambda gtl1"
40. .1413
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/db_xref="GI:64511"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

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Database

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T 1 - 278-6358-3 -278-6358-3 ent no. 5689912 NERAL INFORMATION US APPLICANT: ELGOYHEN, APPLICANT: BOULTEN, APPLICANT: BOULTEN, JAPPLICANT: CALLFORMAN COUNTRY: USA DIEGO STREET: 4365 EXECUT: SAN DIEGO STREET: AND LEGO STREET: LBM PC COUNTRY: USA DIEGO STREET: LBM PC COUNTRY ABPLICATION UNMBER: FILING DATE: 13-JUL CLASSIFICATION NUMBER: RILEPRAN: G19-677-14 TELEPRANCE CHARACTERISTI LEEPRANCE CHARACTERISTI LEMOTH: 457 amino a TYPE: mino a TYPE: amino acid TYPE: protei	ity serv (LFKI
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APPLICANT: JOHNSON, DAVID S.
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR OFRESPONDENCE ADDRESS:
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SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
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                                                         181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                             201 ARGWKHWVFYSCCPTTPYLDITYHFVMQRL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARGWKHWVFYSCCPTTPYLDITYHFVMQRL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P41 9989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
                                                                                                                                                                     Sequence 3, Application US/08464258B
Patent No. 6013766
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.9
Best Local Similarity 94.8
Matches 199, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 619-677-1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                               92121
                                                                                                                                                    US-08-464-258B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
US-08-464-258B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                       RESULT 3
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              91 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDVVLY: DGDFALVKFTKV.LDYTGHIHHHH 140
61 VDYNLKWNPDDYGGYKKIHIPSEKIWRPDLVLYNNAÜÜDFAIVKFTKVLLQYTGHITWTP 120
                                                                            INFESTOAPLISH THE 180
                                                                                            "ASNEMESGEWVIXE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 PAIFKSYCEIIVTHFPFDEONCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNOIVTTNVRLKQQM 60
                                                                                                                                                                                                                                 Sequence 3, Application US/084 1961

Patent No. 6100046

GENERAL INFORMATION:

APPLICANT: ELGOTHEN, ANA BELEN

APPLICANT: BOULTER, JAMES R.

APPLICANT: HEINEMANN, STEPHEN F.

TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL

TITLE OF INVENTION: ACETYLCHOLINE-GAIED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                              AIN
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Pred. No. 1.6e-112;
6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                              E: GRAY CARY WARE & FREIDENRICH 4365 EXECUTIVE DRIVE, SUITE 1600
                                                           121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYD
                                                                               141 PAIFKSYCEIIVTHFFFDEQNCSMKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,961
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P41 9771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.9%;
94.8%;
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                                                                                                                        181 SRGWKHSVTYSCCPDfr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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ADDRESSEE: GRAY CARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                            201 ARGWKUIVEYSCCPTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / MOLECULE TYPE: protein US-08-471-961-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                               SAN DIEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92121
                                                                                                                                                                                                                   US-08-471-961-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Best Local Simi
Matches 199;
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193 YRGWKHWVYYTCCPDTPYLDITYHFIMQRI 222
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 74.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-09-602-807-2
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SEHETRLVAKLEKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 6%; Score 898; DB 3; Length 449; 74.3%; Pred. No. 1e-90; tive 26; Mismatches 28; Indels
                                                                                 Sequence 2, Application US/08462351
Patent No. 6106840
Patent No. 6106840
Patent No. 6106840
APPLICANT: Sharma, Somesh D. APPLICANT: Clark, Brian R. APPLICANT: Lerch, Bernard L. APPLICANT: Lerch, Bernard L. TITLE OF INVENTION: MHC Conjugates Useful in Ameliorating TITLE OF INVENTION: Autoimmunity NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,351
                                                                                                                                                                                                                                                                                            E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 014058-000242US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/462,351
APPLICATION NUMBER: US/08/462,351
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/210,594
FILING DATE: 23-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,084
FILING DATE: 30-AUG-1990
PRIOR APPLICATION PARE:
APPLICATION NUMBER: US 07/690,840
FILING DATE: 23-APR-1991
PRIOR APPLICATION NUMBER: US 07/690,840
FILING DATE: 13-APR-1991
APPLICATION NUMBER: US 07/690,840
FILING DATE: 14-APR-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity (*... Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-462-351-2
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                      US-08-462-351-2
                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                                                     RESULT 4
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61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFALVKFTKVLLQYTGHITWTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 449;
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74.3%; Pred. No. 1e-90;
tive 26; Mismatches 28; Indels
                                                        GENERAL INFORMATION:
APPLICANT: Sharma, Somesh D.
APPLICANT: Clark, Brian R.
APPLICANT: Lerrch, Bernard L.
APPLICANT: Lerrch, Bernard L.
TITLE OF INVENTION: MHC Conjugates Useful in Ameliorating TITLE OF INVENTION: Autoimmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/602,807
                                                                                                                                                                                                                                      E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 014058-000242US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,084
FILING DATE: 30-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/690,840
FILING DATE: 23-ARR-1991
PRIOR APPLICATION DATA:
APPLICATION UNDER: US 07/869,293
APPLICATION UNDER: US 07/869,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALOGATON NUMBER: US 07/869,293
APPLICATION NUMBER: US 07/869,293
FILING DATE: 14-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111-3834
COMPUTER READABLE FORM:
CMPUTER TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,351
Sequence 2, Application US/09602807
Patent No. 6451314
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61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHIWTP 120
                                                                                                                              121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFWESGEWVIKE 180
                                                                                                                                                                                           SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                 APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ANNAPESCEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPEWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Brown, Martin, Haller & McClain
1660 Union Street
                                                                                                                                                                                                                                        181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08 NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: US 07/504,455
                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08487596
Patent No. 6440681
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/POCKET NUMBER: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 03-APR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-NOV-1 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFALVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                        FACENT NO. 5468481

APPLICANT: SHARMA, SOMESH D.;CLARK, BRIAN R.;LERCH, BERNARD L.

TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION NUMBER: 0S/07/367,751
FILING DATE: 21-JUN-189
PRIOR APPLICATION DATA:
RPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.7%; Score 888; DB 6; Length 449;
73.8%; Pred. No. 1.3e-89;
Live 28; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4425-1
atent No. 5194425
APPLICANT: SHARMA ,SOMESH D.;LERCH, L. BERNARD;CLARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 74.3%; Score 896; DB 6;
Matches 156; Conservative 26; Mismatches 28
181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                193 YRGWKHWVYYTCCPDTPYLDITYHFINGRI 222
                                                                                                                                                                     NAMELORIATING AUTOIMMUNITY
NUMBER OF SEQUENCES: 7
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/07/869, 293
FILING DATE: 14-APR-1992
APPLICATION NUMBER: 690, 840
FILING DATE: 23-APR-1991
APPLICATION NUMBER: 576, 084
FILING DATE: 23-AUN-1980
APPLICATION NUMBER: 210, 594
APPLICATION NUMBER: 310, 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 73.8'
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGIH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 449
                                                                           RESULT 6
5468481-1
;Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      5468481-1
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APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                           61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                    PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                               1 SEHETRLVAKLEKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: 16-JUL-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.1%; Score 595.5; DB 2
50.5%; Pred. No. 2.8e-57;
1ve 42; Mismatches 61
  Mismatches
                                                                                                                                                                                                                                                                                  181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                          NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/POCKET NUMBER: P41 9368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-WAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08700636 Patent No. 5910582 GENERAL INFORMATION:
42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 50.5
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-700-636-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
  Matches 106;
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-08-700-636-4
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APPLICANT: Elliot, Kathryn J.
APPLICANT: Elliot, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
                                                                                                                                                                                                                                               61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                        121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                              1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                   1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 504;
                                                             Length 504;
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 595.5; DB 2;
Pred. No. 2.8e-57;
                                                         Query Match 52.3%; Score 597.5; DB 4; Best Local Similarity 51.4%; Pred. No. 1.7e-57; Matches 108; Conservative 40; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                      181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DAS CURRENT APPLICATION NAMER: US/08/466,589 FILING DATE: June 5, 1995 CLASSIFICATION: 536 PRIOR APPLICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6362-9950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FTLING DATE: MAICH 8, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08466589 Patent No. 5837489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 630
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA COUNTRY: USA ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM COMPALLIDE OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ Version 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.1%;
50.5%;
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LENGTH: 504 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-466-589-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
; MOLECULE TYPE: protein US-08-487-596-4
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Best Local Similarity
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US-08-466-589-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 50.5%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: single
unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                   US-09-217-345-4
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                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
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61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                  121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                              APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: Brown. Markit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 VDYNLKHNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHIWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SEHETRLVAKLEKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTENVRLKQQW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.1%; Score 595.5; DB 3; 50.5%; Pred. No. 2.8e-57; tive 42; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                      E. Brown, Martin, Haller & McClaim
1660 Union Street
                                                                                                                            181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FSELSEQ Version 1.5
SOFTWARE: FSELSEQ Version 1.5
APPLICATION NUMBER: US/08/467,574
CLASSIFICATION NUMBER: US/08/467,574
CLASSIFICATION DATA:
APPLICATION DATA:
FILING DATE: MAICH 8, 1993
ATTORNEY AGENT INFORMATION:
FILING DATE: MAICH 8, 1993
ATTORNEY AGENT INFORMATION:
RESERRANCE/OCKET NUMBER: 33,779
TELECOMMUNICATION NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                     Sequence 4, Application US/08467574; Patent No. 6022704
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 504 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 504 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619-238-0062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 50.5
Matches 106; Conservative
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MOLECULE TYPE: protein
US-08-467-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                                      San Diego
                                                                                                                                                                                                                       US-08-467-574-4
                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
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APPLICANT: Elliot, Kathryn J.
APPLICANT: Ellis, Steven B.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
AUDMESSEE: Heller Rham. 61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120 121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180 1 SEHETRLVAKLEKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNOIVTTNVRLKQQW 60 1; Gaps 52.1%; Score 595.5; DB 4; Length 504; 50.5%; Pred. No. 2.8e-57; Live 42; Mismatches 61; Indels 1 ADDRESSEE: Heller Ehrman White & McAuliffe STREET: 4250 Executive Square, 7th Floor 181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210 OPERATING SYSTEM: DOS
SOFTWARE: FSASESD Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/09/217,345
PRIOR APPLICATION DATA:
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/467,574
PRIOR APPLICATION DATA:
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/466,589,
PRIOR APPLICATION DATA:
FILING DATE: 05-JUN-95
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-93
APTONEY/AGERT INFORMATION:
NAME: Seldman, Stephanie I NAME: Selfman, Stephanie L REGISTRATION NUMBER: 33,779 REFERNCE/DOCKET NUMBER: 24735-9949B TELECOMMUNICATION INFORMATION: Sequence 4, Application US/09217345 Patent No. 6303753 GENERAL INFORMATION: APPLICANT: Elliot, Kathryn J. ô

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121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . |||||| |:| ||:|||| || ||:|| ||:|| ||:|| |:| |:| |:| ||: |||| |:| |:| ||:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:
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                                                                                      Patent No. 6013766
GENERAL INFORMATION:
APPLICANT: ELGOVHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: HEINEMANN, STEPHEN F.
ADDRESSES: GRAY CARY WARE & FREIDENRICH LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: GRAY CARY WARE & FREIDENRICH LLP 4365 EXECUTIVE DRIVE, SUITE 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 0530
PRIOR APPLICATION: DATA:
APPLICATION: DATA:
APPLICATION: DATA:
ATTORNEY/AGENT INFORMATION:
NAME: REITER: STEPHEN: E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:

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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                        Sequence 5, Application US/08464258B Patent No. 6013766
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Patent No. 6100046
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: SAN DIEGO
STATE: CALIFORNIA
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US-08-464-258B-5
US-08-464-258B-5
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US-08-471-961-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOUJTER, JAMES R.
APPLICANT: HEINEMANN STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 497;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21.-UL-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
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                                                                                                                                                   181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                      211 APGYNHDIKYNCCEEI-YPDITYSLIIRRL 239
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NAME: REITER, STEPHEN E.
REGIESTRANCHON NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08278635B Patent No. 5683912
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INFORMATION FOR SEQ ID NO: 5:
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amino acid
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STATE: CALIFORN
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PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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APPLICANT: BOULTER, JAMES R.
APPLICANT: HINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
TOTHER OF SEQUENCES: 8
CORRESPONDENCES: 8
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
CITY: SAN DIEGO
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 52.0%; Score 594.5; DB 3; Length 497;
Best Local Similarity 51.4%; Pred. No. 3.6e-57;
Matches 108; Conservative 39; Mismatches 62; Indels 1
                                                                                                                                                                                                                                              COMPUTER: IN P. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/471,961
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-701-194
ATTORNEY AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 941 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
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204 APGYKHEIKYNCCEEI-YQDITYSLYIRRL 232
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Job time : 38 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-677-1405
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 497 antho acids
TYPE: amino acid
                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-961-5
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Human neuronal nic Alpha4 subunit of Alpha4 subunit of Neuronal nicotinic DNA encoding novel Human neuronal nic

Alpha 2 subunit of Neuronal nicotinic Prostate cancer-as Neuronal nicotinic

Human neuronal nic acetylcholin

Drosophila melanog Drosophila melanog Neuronal nicotinic Human CHRNB2 codin Human mutant neuro

Human neuronal nic Neuronal nicotinic Neuronal nicotinic Human neuronal nic Modified acetylcho

Human CHRNB3 gene

Minimum DB s Maximum DB s

Database

26459786

Result Š.

earched:

Modified acetylcho Modified hen ACR s

Human acetyl chol1

OM nucleic

Run on:

Sednence:

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Human; acetylcholine receptor; AChR; immune response; allergy; antibody-mediated disease; gene replacement therapy; T cell epitope; dermatological; immunosuppressive; antiinflammatory; haemostatic; antiallargic; antialtergic; antiathmatic; antithyroid; antidiabetic; autoimmune disease; allergic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "acetylcholine receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human acetylcholine receptor nucleotide seguence.
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                                                                                                                                                                                    ABL10275
ABL11821
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AAS15343
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AAQ14288
AAL45864
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AAQ99348
AAT48238
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AAK92165
AAV12200
AAT59527
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AAT48237
AAS91552
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AAN50415
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AAT48240
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AAV72832
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AAV12199
AAQ90387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ38821 standard; cDNA; 1667 BP
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 Homo sapiens
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 Human acetylcholin
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Alpha subunit of T
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                                                                              ; Search time 300 Seconds
(without alignments)
4729,196 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                       N. Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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Compugen Ltd.
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            GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
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Insect nicotinic A Alpha-9 nicotinic Neuronal nicotinic Drosophila melanog Human TRICH-6 cDNA

Human nicotinic ac Modified acetylcho Modified hen ACR s Mature alpha nicot 529 AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCCATCAACCCG 588

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The present invention describes a method for preventing or inhibiting an indication or disease associated with aberrant, pathogenic or undesirable antibody production, particularly autoimmune or allergic diseases. The method comprises administering a T cell epitope peptide. The sequence of the epitope peptide comprises an immunodominant T cell epitope sequence of the immunodominant T cell epitope sequence. The method can be used to specifically tolerise or down requisite the priming or activity of antigen specific T cells of a mammal. It can be used to prevent or inhibit an indication or disease associated with antibody production to an antigen such as an endogenous antigen, e.g. acetylcholine receptor, insulin, growth hormone, factor VIII or factor IX, or an exogenous antigen e.g. a fungal antigen, a plant antigen, an antigen of a dumestic cat or an antigen of a mit. It can be used to treat autoimmune diseases, e.g. myasthenia gravis, systemic lupus erythematosus (SLE), Grave's disease, autoimmune haemolytic anaemia, thrombocytopenic purpura, caucoimmune asthma, cryoglobulinaemia, thrombic thrombocytopenic purpura, cused for treating allergic diseases, e.g. allergic sathma, atopic dermatitis, allergic gastreontheropathy, anaphylaxis, cuticaria or angloedema. It can allergic some therapy for treating cathma, atopic dermatitis, allergic gastreontheropathy, anaphylaxis, adamontate and an animication such as hamonphila or diabetes or an indication such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adenosine deamidase deficiency, growth hormone deficiency, insulin deficiency, factor IX deficiency or factor VIII deficiency. The present sequence encodes human acetylcholine receptor which is used in the exemplification of the present invention.
                                                                                                                                                      preventing allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1667 BP; 419 A; 465 C; 371 G; 412 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 6.6e-160; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 628.4;
                                                                                                                                                      Use of I cell epitope peptides for, e.g.
                                                                                                                                                                                                         Example 2; Page 217-219; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Matches 629; Conservative
                                                                           WPI; 2000-038343/03.
                                                                                                     P-PSDB; AAY56386
                          Conti-Fine BM;
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ö 109 TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG 168 CCAGTGGAAGACCACCACCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAGCTC 120 121 ATCAATGTGGATGAAGTAAATCAGATGGTGACAACCAATGTGCGTCTGAAACAGCAATGG 180 GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACT 360 CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAG 420 0; Gaps TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG 60 CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT GTGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATT DB 21; Length 1667; Indels 229 181 289 241 349 301 60 361 469 d d 셤 οq ŏ ò g ö ð

AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCCG 480

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 CCCGTGGAAGACCACCGCCAGGCCGTGGAGGTCACGGTGGGCCTGCAGCTGATACAGCTC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 ATCAACGTGGATGAAGTAAATCAGATCGTGACAACCAATGTTCGTCTGAAACAGCAATGG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides derived from the hACR-alpha gene product have similar immunogenicity to the gene product, and may be useful in the treatment and diagnosis of myasthenia gravis caused by neuropathy in sutoimmune reaction to ACR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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GAAAGCGACCCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAG
                            GAAAGCGACCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAG
                                                         TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCAATGTGGATGAAGTAAATCAGATCGTGACAAACCAATGTGGCGTCTGAAACAGCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New peptide(s) useful in treatment of myasthenia gravis - also in diagnosis, having acetyl:choline receptor-alpha like activities.
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                                                                                                                                                                                                                                                                                                                                                hACR-alpha; myasthenia gravis; MG; neuromyopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6;
                                                                                                                                                                                                                                                                                                                  Calf acetyl choline receptor alpha cDNA seguence.
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                                                                                                                                     ATCACCTACCACTTCGTCATGCAGCGCCTG 738
                                                                                                                   601 ATCACCTACCACTTCGTCATGCAGCGCCTG
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                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                         AAN50416 standard; cDNA; 3649
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               CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAG
                                                                             CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
                                     GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCT
                                              AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCCG
                                                                                                                                   GAAAGCGACCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAG
                                                                                                                                                                 TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poly:peptide(s) modulating auto:immune response to acetyl:choline receptor. - comprise all or part of extracellular domain of human acetyl:choline receptor alpha-sub:unit, useful in treatment and diagnosis of myasthenia gravis.
                                                                                                                                                                                                                                                                                                         Human acetylcholine receptor alpha-subunit variant 1 encoding DNA
                                                                                                                                                                                                                                                                                                                        Human; acetylcholine receptor alpha-subunit; hAChR; variant;
myasthenia gravis; autoimmune response; neuromuscular disorder;
diagnosis; ss.
                                                                                                                                                                                                            ATCACCTACCACTTCGTCATGCAGCGCCTG 630
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                                                                                                                                                                                                                                                          AAV72829 standard;
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With a suitable carrier in pharmaceutical compositions, and is useful for such therapeutic (especially masal or oral) administration and diagnosis. MG is a human neuromuscular disorder, in which automatibodies against AChR bind to the receptor and interfere with signal transmission from nerve to muscle at the neuromuscular junction. The extracellular chomain of the AChR alpha-subunit appears to be the prime target for these autoantibodies, particularly the main immunogenic region (MIR). The protein enables antiger specific immunotherapy which suppresses only adverse autoimmune responses whilst leaving overall immune system
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                                                                                                                                                                                                                                                     intact, unlike current methods of treating MG using immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGTGGAAGACCACCCCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAGCTC 120
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                                                                                                                                                                                                                                                                                                   specification but has
                                                                                                                                                                                                                                                                         drugs e.g. steroids.
N.B. The present sequence is not given in the specification but has created by the indexer as specified in the claim usin the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 705;
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 705 BP; 177 A; 192 C; 181 G; 155 T; 0 other;
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Pred. No. 1.7e-137;
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Best Local Similarity 89.4
Matches 630; Conservative
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121 ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGGGTGAC 180
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                                                                  181 ATGGTAGATCTGCCACGCCCCAGCTGCGTGACTTTGGGAGTTCCTTTGTTTTCTCATCTG
                                                                                                                    286 GCAGATGGTGACTTTGCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCAC
                                                                                                                                                                                                                                                      GTGGCCATCAACCCGGAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGCGGGGAG
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                                                                                                   ----AGCAATGGGTGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTG
                                                                                                                                                                  226 AAAAAAATTCACATTCCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGAT
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P-PSDB; AAW83383.
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by the indexer as specified in the claim usin the sequences
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                                                                                                                  numan; acetylcholine receptor alpha-subunit; hAChR; variant;
myasthenla gravis; autoimmune response; neuromuscular disorder;
diagnosis; ss.
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Pred. No. 1.9e-133;
0; Mismatches 0; Indels 79
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AAV72830 standard; DNA; 690 BP
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89.1%;
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Best Local Similarity 89.1
Matches 615; Conservative
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Synthetic.
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The present sequence encodes a human acetylcholine receptor (hAchR)
alpha-subunit variant which is used as all or part of a protein for
modulating the autoimmune response of an individual to hAchR. The
modulating the autoimmune response of an individual to hAchR. The
protein can be administered to alleviate and/or treat mysathenia gravis
(MG), and is useful for diagnosing the condition. It can be combined
if the suitable carrier in pharmaceutical compositions, and is useful
for such therapeutic (especially nasal or oral) administration and
diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
diagnosis. MG is a human neuromuscular disorder, in which autoantibodies
against AchR alpha-subunit appears to be the prime target for
commain of the AchR alpha-subunit appears to be the prime target for
these autoantibodies, particularly the main immunogenic region (MIR).
The protein enables antigen-specific immunotherapy which suppresses only
adverse autoimmune responses whilst leaving overall immune system
intact, unlike current methods of treating MG using immunosuppressive
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                                                                                                                                                                                                                                                                                                                                                                                   drugs e.g. steroids. N.B. The present sequence is not given in the specification but has been created by the indexer as specified in the claim usin the sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CCAGTGGAAGACCACCGCCAGGTCGTGGTCACCGTGGGCCTGCAGCTGAAAACAGCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
acetyl:choline receptor alpha-sub:unit, useful in treatment and diagnosis of myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 363 BP; 104 A; 88 C; 91 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 363; DB 19; 
; Pred. No. 2.2e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acetylcholine receptor alpha subunit mRNA
                                                         -; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT06284 standard; mRNA; 1350 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 363; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               given in the figures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                         Claim 9iii; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCA 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT06284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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CCAGTGGAAGACCACCGCCAGGTCGTGGAGGTCACCGTGGGCCTTGCAGCTGATACAGCTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GTGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAAATTCACATT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 AUUGANGBAGGCUUCGCUGGAAUCCAGCCGAUUAUGGUGGAAUUAAAAAAGAUCAGACUG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||::| || | ::||| || ||| :|:| || ||| 336 CUUCUGAUGAUGUUGGCUGAUUUU 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAUUGUUCACAUGACCAAACUGCUUUUGGAUUAUACGGGAAAAAUAAUGUGGACACCU 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGCCTCTGTCGTGGCCATCAACCCG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 UCUGAACAUGAAACACGUUUGGUUGCUAAUUUAUUAGAAAAUUAUAAAAAGGGGGUGAUUCGU 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The mRNA sequence given in AAT06284 codes for the alpha subunit the electric ray acetylcholine receptor (AChR) (AAR86421). AChR is an autoantigen involved in the pathogenesis of myasthenia gravis. AChR peptide segments are used in the construction of MHC class II-peptide conjugates utilised in the treatment of autoimmune diseases, or as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                               non-responsiveness - opt. including a toxin, esp. for treating auto-immune disease such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.2%; Score 354; DB 17; Length 1350; ilarity 54.8%; Pred. No. 1e-85; Conservative 113; Mismatches 170; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1350 BP; 384 A; 243 C; 285 G; 438 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            New MHC Class 2-peptide complex for inducing T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 6; 47pp; English.
allograft rejection; vaccine; ss.
                                                                                                                                                                                                                                                                                                              SD;
                                                                                                                                                                           88US-0210594.
89US-0367751.
90US-0576084.
90US-0635840.
91US-0690840.
                                                                                                                                                                                                                                                                                                              Sharma
                                                                                                                                                                 92US-0869293
                                                                                                                                 88US-0210594
                                Torpedo californicus
                                                                                                                                                                                                                                                                                                              Clark BR, Lerch BL,
                                                                                                                                                                                                                                                                              (AMER-) AMERGEN INC.
                                                                                                                                                                                                                                                                                                                                           WPI; 1996-010049/01.
P-PSDB; AAR86421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 343; Conserv
                                                                                                                               23-JUN-1988;
                                                                                                                                                                                                             30-AUG-1990;
28-DEC-1990;
                                                                                                                                                                                                                                             23-APR-1991;
                                                                JS5468481-A.
                                                                                                21-NOV-1995
                                                                                                                                                                 14-APR-1992;
                                                                                                                                                                              23-JUN-1988)
21-JUN-1989)
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DB 14; Length 1350;

9 96 120 156 180 240 276 300 336 360 396 420 480

540 576

Location/Qualifiers

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sig_peptide

Key

Synthetic

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541 TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC 600
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binding site; MHC; IAB; alpha; beta; RAMPS; Torpedo californicus; ss.
                                                                                                                                                                                                                                                                                                            1 TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG
                                                                                                                                                                                                                            61 CCAGTGGAAGACCACCGCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAGCTC
                                                                                                                                                                                                                                                                                                                                                                  121 ATCAATGTGGATGAAGTAAATCAGATGGTGACAACCAATGTGCGTCTGAAACAGCAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              481.GAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCCG
system which are responsible for undesirable immune responses. may be used for treating autoimmune disease such as rheumatoid arthritis, multiple sclerosis or myesthnia gravis.
                                                                                                                                                                Matches 343; Conservative 113; Mismatches 170; Indels
                                                                                 Sequence 1350 BP; 384 A; 243 C; 284 G; 435 U; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha subunit of Torpedo californicus AChR (known).
                                                                                                                      56.1%; Score 353.6; DB 154.8%; Pred. No. 1.3e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:|||||:||||| :: :||:|||||||| aucaccuaccauuuuuaucaugcagcg 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 ATCACCTACCACTTCGTCATGCAGCG 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ35053;
                                                                                                                        Query Match
                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence shows the mRNA for the alpha subunit of acetylcholine receptor protein. This sequence may be used in the construction of an MHC-peptide complex which comprises an antigenic peptide, eg. ACHR peptide 195-215 or myelin basic protein peptide MBP(1-14)A4, and an isolated MHC subunit component which has an antigen binding site, where the antigenic peptide is associated with the antigen binding site. The MHC-peptide complex selectively binds a T-cell receptor on T-cells associated with diseases, esp. autoimmune diseases. This subunit derived from the MHC antigen. The incorporated in the asequence encoding the subunit derived from the MHC antigen. The incorporated site will be such that, when the subunit is expressed and folded, the ACHR peptide antigen will be available as an epitope for the target T-cells. The complex may be used to identify and inhibit aspects of the immune
                                                                                                                                         541 TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acetylcholine receptor; AChR; epitope; myasthenia gravis; human; MHC; mouse; MHC-peptide complex; subunit; antigen; binding site; receptor; T-cell; autoimmune disease; immune system; rheumatoid arthritis;
                                                              AAUUGCACUAUGAAGUUGGGAAUCUGGACGUACGAUGGGACAAAAGUUUCCAUAUCCCCG
                                         GAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complexes comprising antigenic peptide and major histocompatibility complex sub-unit - for treatment and diagnosis of immune diseases, e.g. rheumatoid arthritis, multiple sclerosis and myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acetylcholine receptor protein, alpha subunit mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sharma SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple sclerosis; myesthnia gravis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1..36
4.tag= a
37..1350
/*tag= b
                                                                                                                                                                                                 601 ATCACCTACCACTTCGTCATGCAGCG 626
                                                                                                                                                                                                                        AAQ39941 standard; mRNA; 1350 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nag
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark BR, McConnel HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-182250/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ANER-) ANERGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAR36984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                        24-SEP-1993
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sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                  The Dupont apparatus and technique for rapid multiple peptide synthesis (RAMPS) is used to synthesise the members of a set of overlapping (10 residue overlap), 20 residue peptides form the alpha subunit of Torpedo californicus ACHB.

The ACHR peptide 195-215, which has been characterised as an epitope in myasthenia gravis (MG) in humans and in mice, may be connected to the N-terminal antigen binding site of a polypeptide derived from an MHC antigen associated with MG. For example, if the recombinant complex is to be used in mice, the AChR peptide may be incorporated into a sequence encoding either the I-Ab-alpha or I-Ab-beta chain (see AAQ13504-55 respectively). If the AChR peptide is to be incorporated into the beta chain, for example, the oligonucleotide may be inserted as a replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GTGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCT 360
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                                                                                                                                                                                                                                                                                          Pure major MHC-peptide complex - useful in treating deleterious Immune response such as auto:immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 14; Length 1350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.9%; Score 352.4; DB 14; Length Best Local Similarity 54.6%; Pred. No. 2.8e-85; Matches 342; Conservative 113; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1350 BP; 384 A; 247 C; 281 G; 438 U; 0 other;
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                                                                                                                                                                                                             SD;
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                                                                                                                                             91US-0690840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the leader sequence.
                                                                                                                                                                                                             Lerch BL,
                                                                                                                                                                           ANER-) ANERGEN INC
                                                                                                                                                                                                                                           WPI; 1993-036056/04
                                                                                                                                                                                                                                                            P-PSDB; AAR35057
                                                                                                                                           23-APR-1991;
                                               WO9218150-A
                                                                               29-0CT-1992
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457 AAUUGCACUAUGAAGUUGGGAAUCUGGACGUACGAUGGGACAAAAGUUUCCAUAUCCCCG 516
                                             CCAGTGGAAGACCACCGCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAGCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The acetylcholine receptor alpha subunit given in sequence AAR45946 (corresponding mRNA in AAQ56918) and the myelin basic protein given AAR45947 are antigenic peptides associated with autoantigens. They have been conjugated with MHC class II components such as I-Ab-apha chain (encoded by sequence AAQ56919) or I-Ab-beta chain (encoded by AAQ56920) and a toxin or label to form conjugates used to target helper I-cells for the treatment of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG
                              GAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGAG
                                                                                    541 TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCGACACCCCCTACCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC-mediated toxic peptide conjugates - useful for ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15; Length 1350;
                                                                                                                                                                                                                                                                                                                                                    MHC; major histocompatibility complex; toxic conjugate; autoimmunity; autoimmune disease; helper T-cell; T-lymphocyte; acetylcholine receptor; myelin basic protein; I-Ab; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1350 BP; 384 A; 244 C; 285 G; 437 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.8%; Score 326.6; DB 15; larity 54.4%; Pred. No. 2.6e-78; Conservative 112; Mismatches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 6.1-6.4; 42pp; English.
                                                                                                                                                                                                                                                                                                                             Acetylcholine receptor alpha subunit.
                                                                                                                                                            ВР
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                                                                                                                                             ATCACCTACCACTTCGTCATGCAGCG
                                                                                                                                                                                                                                           AAQ56918 standard; mRNA; 1350
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90US-0576084.
90US-0635840.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-056406/07.
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30-AUG-1990;
28-DEC-1990;
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                                                                                                                          GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACAT---CACGTGGACA 357
                                                                                                                                                                 CCTCCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCCACTTTCCCTTTGATGAA 417
                                                                                                                                                                                                        CAGAACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAAC 477
                                                                                                                                                                                                                                                                           CCGGAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAG 537
                                                                                                                                                                                                                                                                                       GAGTCCCGGGGCTGGAAGCACTCCGTGACTATTCCTGCTGCCCCGACACCCCCTACCTG 597
                                           ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGG
                                                                                                             CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
                                                                                                                                                                                                                                             Human acetylcholine receptor alpha-subunit variant 4 encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poly:peptide(s) modulating auto:immune response to acetyl:choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; acetylcholine receptor alpha-subunit; hAChR; variant; myasthenia gravis; autoimmune response; neuromuscular disorder;
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P-PSDB; AAW83384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; ss
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Synthetic.
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The present sequence encodes a human acetylcholine receptor (hAChR)

alpha-subunit variant which is used as all or part of a protein for

modulating the autoimmune response of an individual to hAChR. The

protein can be administered to alleviate and/or treat myasthenia gravis

(MG), and is useful for diagnosing the condition. It can be combined

vith a suitable carrier in pharmaceutical compositions, and is useful

for such therapeutic (especially masal or oral) administration and

diagnosis. MG is a human neuromuscular disorder, in which autoantibodies

against AChR bind to the receptor and interfere with signal transmission

from nerve to muscle at the neuromuscular junction. The extracellular

domain of the AChR alpha-subunit appears to be the prime target for

these autoantibodies, particularly the main immunogenic region (MIR).

The protein enables antigen-specific immunotherapy which suppresses only

adverse autoimmune responses whilst leaving overall immune system

contact, unlike current methods of treating MG using immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                     drugs e.g. steroids.
N.B. The present sequence is not given in the specification but has been created by the indexer as specified in the claim usin the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 GCAGATGGTGACTTTGCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCAC
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receptor - comprise all or part of extracellular domain of human acetyl:choline receptor alpha-sub:unit, useful in treatment and diagnosis of myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.1%; Score 278; DB 19; Length 438; 82.9%; Pred. No. 2.4e-65; Live 0; Mismatches 0; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 438 BP; 116 A; 106 C; 113 G; 103 T; 0 other;
                                                                          Claim 9iv; Fig -; 58pp; English.
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Matches 363; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human acetylcholine receptor (hAchR) alpha subunit variant which is used as all or part of a protein for modulating the autoimmune response of an individual to hAchR. The protein can be administered to alleviate and/or treat myasthenia gravis (MG), and is useful for diagnosing the condition. It can be combined with a suitable carrier in pharmaceutical compositions, and is useful for such therapeutic (especially masal or oral) administration and diagnosis. MG is a human neuromuscular disorder, in which autoantibodies against AChR bind to the receptor and interfere with signal transmission from merve to muscle at the neuromuscular junction. The extracellular choman interfere which signal transmission from merve to muscle at the neuromuscular junction. The extracellular choman contraction and interfere with signal transmission choman of the AChR alpha esubunit appears to be the prime target for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drugs e.g. steroids. N.B. The present sequence is not given in the specification but has been created by the indexer as specified in the claim usin the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              these autoantibodies, particularly the main immunogenic region (MIR). The protein enables antigen-specific immunotherapy which suppresses only adverse autoimmune responses whilst leaving overall immune system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                364 GCCATCTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAGAAC 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 TGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCCGGAA 483
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Human acetylcholine receptor alpha-subunit variant 5 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poly:peptide(s) modulating auto:immune response to acetyl:choline receptor - comprise all or part of extracellular domain of human acetyl:choline receptor alpha-sub:unit, useful in treatment and diagnosis of myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; acetylcholine receptor alpha-subunit; hAChR; variant;
myasthenia gravis; autoimmune response; neuromuscular disorder;
diagnosis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.4%; Score 267; DB 19;
100.0%; Pred. No. 1.9e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            Souroujon MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9v; Fig -; 58pp; English.
                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                             98WO-IL00211.
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                                                                                                                                                                                                                                                                                                                                                            Barchan D, Fuchs S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 given in the figures.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-610383/51.
P-PSDB; AAW83385.
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                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product "neuronal nicotinic acetylcholine receptor alpha-2 subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCGTGGTGCGGC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; neuronal nicotinic acetylcholine receptor; alpha-2 subunit; brain tissue; screening; NAChR; antibody; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
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                                 Location/Qualifiers
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604 ACCTACCACTTCGTCATGCAGCGCCTG
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                                                                                                                                                                                                                        AAV12199 standard; cDNA; 2277
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                                                                                                    482 AAAGCGACCAGACCTGAGCAACTTCATGGAGAGCGGGAGTGGGTGATCAAGGAGT
         TCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGGG
                                                                                            CTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTTG
                                                                                                                          302 CTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCTC
                                                                                                                                                                                                                                                     CCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGACA
                                                             182 IGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAAATTCACATTC
                                                                            512 GCGACTACAAACTGCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                       Human nNAChr; neuronal nicotinic acetylcholine receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                neurotransmitter; ss.
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                                                                                                                                          DNA encoding the human nNAChR alpha2 subunit was isolated froma human thalamus tissue CDNA library using corresp. rat cDNA. The insert of one clone obtd. was ligated with the insert of another clone to generate a full-length alpha 2 subunit cDNA. The DNA can be used to identify function nNAChRs. Cells contg. the DNA can be used for screening to identify cpds. which modulate the activity of human nNAChRs. The human nNAChR alpha 2 subunit can be used to product antibodies which can be used in immunohistochemistry, diagnosis and therapy. The nucleic acids can be used for analysing disease states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 CAGTGGAAGACCACCCCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAGCTCA 121
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New human neuronal nicotinic acetylcholine receptor alpha2 subunit used to develop prods. for detection, diagnosis and therapy and for modulating activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 CAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 ACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGCTCTGTCGTGGCCATCAACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.6%; Score 224.2; DB 16; 60.9%; Pred. No. 1.6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACCTACGCCTTCGTCATCCGGCGGCTG 957
                                                                                               Claim 2; Page 43-46; 54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                and creating animal models
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Matches 383; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Title: Perfect score:

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AA596914 vo21f03.r

AA635688 Vu22602.r

BE664308 148713 MA

AA636794 vr16612.r

AA636687 vr155f05.r

BO735223 AGENCOURT

BA053522 AGENCOURT

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BU03620897 NISC_n107

BU040944 BU06944

BU065441 BU065441

BU06532 BU06932

BU06932 BU06932

BU075194 BU0991265

BU06932 BU06932

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BU07186 BU09932 BU09934

BU07186 BU09938 BU099994 GU3944157

AW714206 EST745510
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BB653265 BB653265
BB639700 BB639700
ALILO117 GH09582.5
BB665088 BB665088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ota'T., Nishikawa'T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helix Research Institute
1532-3 Yana, Kisrazu, Chiba 292-0812, Japan
151: 81-438-52-3975
Fax: 81-438-52-3986
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BJ062941
BJ0629431
BG828551
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BJ069932
BJ069932
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BJ06841
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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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KEYWORDS
SOURCE
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AUTHORS
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BF305214 601892667
BF307986 601894231
BB613689 BB613689
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Copyright (c) 1993
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80.2
79.3
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Score

Result 2 617.4 548.2 519.6 505.2 499.6

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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM1840 row: p column: 22
High quality sequence stop: 696.
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                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5021829"
                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="NIH_MGC_17"
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1. .837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI114221 837 bp mRNA linear EST 26-JUN-2001 602862588F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:5021829 5',
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Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500
                                                                                                                                                                                                                                                                                                                                                                                61 CCAGIGGAAGACCACCGCCAGGICGIGGAGGICACCGIGGGCCIGCAGCIGAIACAGCIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGG 180
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/dev_stage="embryo, 10 weeks"
/note="vector: pmE18SE13"
/note="vector: pmE18SE13"
) a 249 c 214 g 198 t 3 others
                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                Query Match 98.0%; Score 617.4; DB 9; Best Local Similarity 99.7%; Pred. No. 5e-158; Matches 629; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                            , 1;
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1. .864
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following 5' adaptor: GGCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF305214 806 bp mRNA linear EST 21-NOV-2000 601892667F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138360 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1047 row: e column: 17
High quality sequence stop: 680.
Location/Qualifiers
1. .806
                                                            481 GAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGCGGGGGAGTGGGTGATCAAGGAG 540
                                                                                                                                                                                                                                                                                                                                                                                                 301 GIGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATT 360
                                                                                                                                                                                                                                                                                         421 AACTGCAGCATGAAGCTGGGCACCTGGACCTAACGACGCTCTGTCGTGGCCATCAACCCG 480
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases to 806)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
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/clone="InBoTe"
/tissue_type="rhabdomyosarcoma"
/lab_host="NHIOB (phage-resistant)"
/note="Organ: muscle; Vector: POTB7; Site_1: EcoR1;
Site_2: Xhoi; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the
                                                                                                                                              CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCCACTTTCCCTTTGATGAACAG
                                           241 CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
                                                                                                                         301 GCTATIGICAAGTICACCAAAGIGCICCIGCAGIACACIGGCCACATCACGIGGACACCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.2%; Score 505.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence. BF305214
BF305214 GI:11252076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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JOURNAL
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AUTHORS
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BF305214
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E I (bases 1 to 713)

E II (bases 1 to 713)

I (bases 1 to 713)

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM1009 row; p column: 23

High quality sequence stop: 711.
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Site_2: XhOI; CDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                BF309251 713 bp mRNA linear EST 21-NOV-2000 601890196F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4124038 5',
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               541 TCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGCCCCGACACCCCCTACCTGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTAAAGACTACAGCAGCGTGGTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12;
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Pred. No. 2.7e-131;
0; Mismatches 14;
                                                                                                                         601 A-TCACCTACCACTTCGTCATGCAGCGCCTG 630

    713
    /organism="Homo sapiens"
/db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                     mRNA sequence.
BF309251
BF309251.1 GI:11256573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.5%;
ilarity 96.9%;
Conservative
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Local

Best Loc Matches

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/note="Organ: muscle; Vector: porB7; Site_1: EcoRI; Site_2: XhoI; CDNA made by Oligo-dT priming.
Site_2: XhoI; CDNA made by Oligo-dT priming.
Directionally cloned into EcoRI/Anis sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB613689 RIKEN full-length enriched, 0 day neonate head Newtolius CDNA clone 4831406609 5', mRNA sequence.
BB613689 1 GI:15395640
                                                                                                                                                                                                                                                                                                                    Length 660;
                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                            /lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                Score 499.6; DB 12
Pred. No. 7.7e-126;
0; Mismatches 4;
                      /clone="IMAGE:4140078"
/clone_lib="NIH_MGC_17"
/tissue_type="rhabdomyosarcoma"
                                                                                                                                                                                                                                                                                                                  79.3%;
98.5%;
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                      Similarity
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KEYWORDS
SOURCE
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BB613689
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                      3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outract: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ArC.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCMAGSI row: m column: 07

High quality sequence stop: 658.

Location/Qualifiers
                                                                              CCAGTGGAAGACCACGCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAGCTC 120
                                                                                                                                                                                                               ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGG 180
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 660)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                      Gaps
                                                          TCCGAACATGAGACCCGTCTGGTGGCAAAGCTATTTAAAGACTACAGCAGCGTGGTGCGG 60
                                                                                                                                                           GTGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATT
                                                                                                                                                                                                                                                                                                                                                                      CCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTTT
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2.5e-127;
ches 13;
Pred. No. 2.5e
); Mismatches
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/organism="Homo sapiens"
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  96.88;
l Similarity 96.8
548; Conservative
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BF307986
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LOCUS

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ESSION SION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

JOURNAL

TITLE COMMENT

480

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31-AUG-2001 Mus

source

FEATURES

COMMENT

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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
      O
                                                              Query Match 73.6
Best Local Similarity 88.4
Matches 503; Conservative
    172
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  BASE COUNT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa
.Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa
.K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,
Ishil, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                   Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratcry Yof Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                  Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,Y.,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3']. CDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from IsanAs FIT I "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, 0 day neonate
1 (bases 1 to 651)
Arakawa,T., Carninci,P., Fukuda,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .651
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="4831406G09"
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                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
                     AUTHORS
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FEATURES

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Mus musculus
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 566)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geislanberg,K., Steptoe,M., Te,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Materston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA596914 566 bp mRNA linear EST 19-SEP-1997 vo21f03.rl Barstead mouse myotubes MBLRBS Mus musculus CDNA clone IMAGE:1050557 5' similar to 9b:MJ7640 Mouse acetylcholine receptor alpha-subunit mRNA (MOUSE); mRNA sequence.
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                                                                   DB 10; Length 651;
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Contact: Marra M.Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                              Score 463.4; DB 1C
Pred. No. 6.2e-116;
0; Mismatches 66;
142
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                                                                   73.68;
88.48;
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548 AGCTCGGGGCTGGAA 562

g

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AA755688 1100-21 Barstead mouse myotubes MPLRB5 Mus musculus CDNA clone IMAGE:1180443 5' similar to 99:Y00762 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA CHAIN PRECURSOR (HUMAN); 9b:X03986 Mouse mRNA for muscle nicotinic acetylcholine receptor (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3']; double-stranded cDNA was ligated to Eco RI adaptors [AATYCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library constructed by Bob Barstead. The C2C12 call line (available from ATCC, catalog # CRL-1772) differentiates
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 946) Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Email: mouseest@watson.wustl.edu
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85.4%; Pred. No. 2.2e-109;
iive 0; Mismatches 87;
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rapidly, forming contractile my
characteristic muscle proteins.
248 c 242 g 224 t
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C3H"
/db_xref="taxon:10090"
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AA755688.1 GI:2802886
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                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                               house mouse.
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                                                              RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 CATCAATGTGGATGAAGTAAATCAGATCGTGACCAATGTGCGTCTGAAACAGCAATG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 GGTCGATTACAACTTGAAATGGAATCCAGATGACTATGGAGGAGTGAAAAAAATTCACAT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 TCCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACA 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCGAACATGAGACCCGTCTG-GTGGCAAAGCTATTTAAAGACTACAGCGGGGGTGGTGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 TCCTTCAGAAAAGATCTGGCGCCCAGACCTTGTTCTCTATAACGATGCAGATGGTGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 566;
                                                                                                                                                                                                                                                                                              /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                    Score 448.6; DB 9;
Pred. No. 6.5e-112;
0; Mismatches 59;
                                                                                                                                                                                                                                /strain="C3H"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                          /clone="IMAGE:1050557"
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89.2%;
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Matches 495; Conservative
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Bovidae; Bovinae; Bos.

I (bases 1 to 554)

Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casass, E., White, J., Cho, T., Farents, A.J., Chitko-Neckow, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Neckow, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                      308
                                                                                                                  419
189 TATCAATGTGGATGAAGTAAATCAGATTGTGACCAATGTACGTCTGAAACAGCAATG 248
                                                                                                                                                                                                                                                                          547
                                                                                                                                                                                                                                                                                                                                                                                                                GAACTGCAGCATGAAGCTGGGCACCTGGACCTACGACGGCTCTGTCGTGGCCATCAACCC 479
                                                                                                                                                                                                                                                                                                                                                                                            GGAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGGA 539
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                                               300 TGCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCCACATCACGTGGACACC
                                                                                                                                                                                                                                                        360 TCCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE664308 554 bp mRNA linear linear H8713 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. BE64308.1 GI:10023661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTE1: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACATCACCTACCACTTCGTCATGCAGC 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTCCCAGTCACGACG
Plate: 53 row: N column: 4
Seq primer: ATTTAGGTGAAACTATAG.
Location/Qualifiers
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FORWARD: AGGAAACAGCTATGACCAT
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AUTHORS
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BE664308
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VIIGUL:1 Barstead mouse myotubes MPLKB5 Mus musculus cDNA clone IMAGE:1120823 5' similar to gb:MI7640 Mouse acetylcholine receptor Alpha-subunit mRNA (MOUSE);, mRNA sequence.
AA636794
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 497)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                                                                                                                             ö
1. .554
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4B0V"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCWY SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               152 CCCGTGGAAGACCACCCCAGGCCGTGGAGTCACGTGGGCCTGCAGCTGATACAGCTC
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                                                                                                                                                                                                                                                                  554;
                                                                                                                                                                                                                                                               Query Match 66.4%; Score 418.2; DB 10; Length Best Local Similarity 94.0%; Pred. No. 1.4e-103; Matches 435; Conservative 0; Mismatches 28; Indels
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                  117
                                                                                                                                                                                               135 g
                                                                                                                                                                         embryos."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 479)
Marra, M.; Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theisling, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                AA636687 Linear EST 22-OCT-1997 vrIs505.rl Barstead mouse myotubes MPLRBS Mus musculus CDNA clone IMAGE:1120737 5' similar to 9b:M17640 Mouse acetylcholine receptor alpha-subunit mRNA (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:610073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GGAGTGAAAAAAATTCACATCCCCTCGGAAAAGATCTGGCGGCCGGACGTCGTTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 GGTGTGAAAAAATTCACATTCCTTCAGAAAAGATCTGGCGCCCCAGACCTTGTTCTCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GTGCGTCTGAAACAGCAATGGGTGGATTACAACCTAAAATGGAATCCAGATGACTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 479;
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 341.
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88.8%; Pred. No. 3.3e
:ive 0; Mismatches
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/clone="IMAGE:1120737"
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1. .479
                                                                                                      AA636687.1 GI:2560466
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Best Local Similarity 88.8
Matches 426; Conservative
                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                 Waterston, R.
                                                                                                                                          house mouse.
                                                                                      AA636687
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KEYWORDS
SOURCE
ORGANISM
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                                                                                  ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ï
                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:610159
Seq primer: -28ml3 rev2 ET from Amersham.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 GTACGTCTGAAACAGCAATGGGTCGATTACAACTTGAAATGGAATCCAGACGACTATGGA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 AACAACGCAGACGGCGACTTTGCCATTGTCAAATTCACCAAGGTGCTCCTGGACTACACC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGTCGTGGCCATCAACCCGGAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGC 519
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   Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 497;
                                                                                                                                                                                     /strain="C3H"
/db_xref="taxon:10090"
/clone="InAGE:1120823"
/clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
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   St.
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Pred. No. 8.9e-97;
0; Mismatches 54
Forest Park Parkway, Box 8501,
                                                                                                                                                     1. .497
/organism="Mus musculus"
                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.4%;
illarity 88.8%;
Conservative
                Tel: 314 286 1800
Fax: 314 286 1810
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Matches 436; Conserv
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BJ064207 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis CDNa clone XL078109 5', mRNA sequence.
BJ064207 I GI:17425045
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Kitayama,A., Terasaka,C., Mochil,M., Ueno,N., Shin-1,T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                             GCTATTGTCAAGTTCACCAAAGTGCTCCTGCAGTACACTGGCCACATCACGTGGACACCT
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                                                                          ATCAATGTGGATGAAGTAAATCAGATCGTGACAACCAATGTGCGTCTGAAACAGCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGCCATCTTTAAAAGCTACTGTGAGATCATCGTCACCCACTTTCCCTTTGATGAACAG
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Contact: Tadasu Shin.i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
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/db_xref="taxon:8355"
/clone="XL078109"
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
181 AACAACGCAGACGTTTGCCATTGTCAAATTCACCAAGGTGCTCCTGGACTACACC 240
                                                                                                                                                                    GGGGAGTGGGTGATCAAGGAGTCCCGGGGCTGGAAGCACTCCGTGACCTATTCCTGCTGC 579
                                                                                                                                                                                                                                                                                                                                                                  80 TCTGAGGATGAATCCCGCCTTAFAAATGACTTATTCAAGAGCTACAACAAAAGTGGTTCGT 139
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                                                                                                                                              CACTTTCCCTTTGATGAACAGAACTGCAGCATGAAGCTGGGCCACCTGGACCTACGACGGC 459
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                                                                          GGCCACATCACGTGGACACCTCCAGCCATCTTTAAAAAGCTACTGTGAGATCATCGTCACC
                                                                                                                                                                                                                                          TCTGTCGTGGCCATCAACCCGGAAAGCGACCAGCCAGACCTGAGCAACTTCATGGAGAGC
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Pred. No. 7.9e-84;
0; Mismatches 177; Indels
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/dev_stage="entropy" Act Engle 31-32"
//dev_stage="enbryo, stage 31-32"
//lab_host="DH10B (phage-resistant)"
//note="Organ: whole embryo; Vector: pCMV-SPORT6; Site_1:
Not; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC
       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution: NCI-CGAP clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbpp/image.html
Plate: LLAMI2318 row: I column: 18
High quality sequence stop: 649.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 CCAGTCAAGGCTTTTAAGGACAAAGTTGTGGTGACGGTGGGACTCCAGCTTATACAGCTT
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Pred. No. 1.2e-83;
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                                                                                                                                                                                                                                                                                                       /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:5572769"
/clone_lib="NICHD XGC Emb4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
                       Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 193 g
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Best Local S:
Matches 452,
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AGENCOURT_8097732 NICHD XGC Emb4 Xenopus laevis cDNA clone
IMAGE:5572769 5', mRNA sequence.
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: Not1; Site_2: EcoRI; cDNAswere cligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amopodinae; Xenopus.
1 (bases 1 to 862)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                            Length
                                                                                                                                                                                                                 Indels
                                                                                                                                                                            DB 13;
                                                                                                                                                                       Score 345.8; DB 13;
Pred. No. 1e-83;
0; Mismatches 177;
                                                                                                 (Wellcome/CRC Institute)
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BQ733592.1 GI:21872489
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71.9%;
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                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                  204
                                                                                                                                                                                                               452;
                                                                                                                  BASE COUNT
ORIGIN
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AUTHORS
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KEYWORDS
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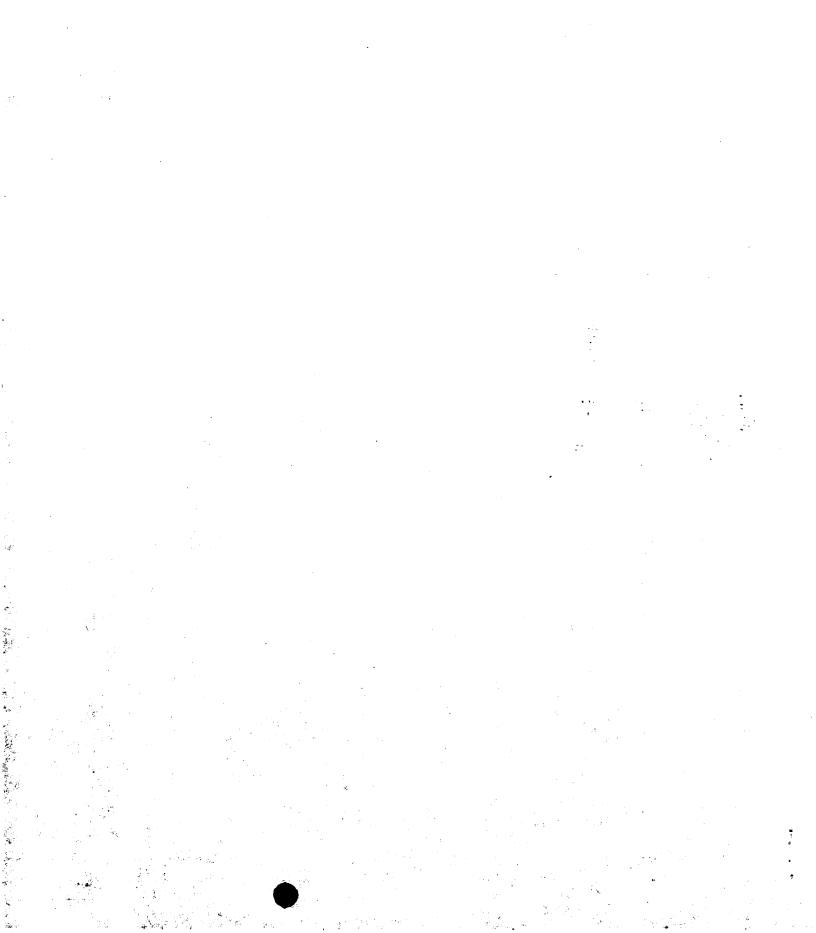
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Search completed: January 14, 2003, 16:48:24 Job time: 2262 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                    EST 12-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 494)
                                                                                                                                                                                                                                                                                       AA688563 494 bp mRNA linear EST 12-DEC-199 vul7b11.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1180893 5' similar to gb:X03986 Mouse mRNA for muscle nicotinic acetylcholine receptor (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRf; Site_2: NotI; ist strand cDNA was primed with a Not I - oligo(dT) primer [5' representation of the continued of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.linl.gov) for further information. MGI:638741
Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CCAGTGGAAGACCACCCCAGGTCGTGGAGGTCACCGTGGGCCTGCAGCTGATACAGCTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Barstead mouse myotubes MPLRB5"
/cell_line="C2C12"
/lab_host="DH10B"
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
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Location/Qualifiers
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/db_xref="taxon:10090"
                                            /clone="IMAGE:1180893"
601 ATCACCTACCACTTCGTCATGCAGCGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA688563.1 GI:2677992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                house mouse.
Mus musculus
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                                                                                                                                                                                                                                                                                                                                   DEFINITION
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JOURNAL
COMMENT
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                                                                                                                                                                                                       RESULT 15
AA688563
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KEYWORDS
SOURCE
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195 ATCAATGTGGATGAAGTAAATCAGATTGTGACAACCAATGTACGTCTGAAACAGCAATGG 254
                                                                                                                                                                     301 GCTATIGICAAGTICACCAAAGIGCTCCIGCAGTACACIGGCCACATCACGIGGACACCT 360
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                                                            GTGGATTACAACCTAAAATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATT
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Acetylcholine rece Acetyl choline acc Alpha subunit of T Acetylcholine rece Fish acetylcholine Human acetylcholin

Human acetylcholin Human neuronal nic

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hACR-alpha; myasthenia gravis; MG; neuromyopathy
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/label= Epitope
/note= "Claim 1 (III)"
181.186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.47
/label- Epitope
/note- "Claim 1 (I)"
86.91
/label- Epitope
/note- "Claim 1 (II)"
158.163
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/label= Epitope

/note= "Claim 1 (V)"

354..359

/label= Epitope

/note= "Claim 1 (VI)"
                                                                                          AAW83383
AAW83384
AAW44156
AAW09022
AAO17245
ABB08885
                                                                                                                                                                                                                                                                                                                                                                              AAW09018
AA017242
ABB08883
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ABB59012
AAW09020
AAE12775
ABB61954
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AAW09024
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/label= Epitope
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   Homo sapiens
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Active-site
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 Human acetylcholin
Human acetylcholin
Human acetylcholin
Calf acetylcholine
Mouse acetylcholin
Chicken acetylchol
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Human acetylcholin
Human Acetylcholin
                                                                                                                           ; Search time 140 Seconds
(without alignments)
199.876 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acenteseq_LO10021**

(SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA1981.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA1983.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA1983.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA1984.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA1986.DAT:*
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(SIDSZ/gcgdata/geneseq-embl/AA1980.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA1980.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA1990.DAT:*
(SIDSZ/gcgdata/geneseq-embl/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                       1 SEHETRLVAKLFKDYSSVVR.....SCCPDTPYLDITYHFVMQRL
                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                           January 14, 2003, 16:10:42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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AAY56386
AAU69151
AAW83381
AAW83382
AAW83382
AAW6255
AAR06255
AAR06255
AAR36984
                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_101002:*
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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1111.5
1100.5
1088.5
1086.5
1074.5
969.5
                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                              Scoring table:
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Neuronal nicotinic Modified acetylcho Insect nicotinic A Modified acetylcho Modified hen ACR s

Modified acetylcho Human neuronal nic Drosophila melanog

nicotinic

Neuronal

Drosophila melanog Drosophila melanog Human cholinergic

JTF-38 nAChR alpha Nicotinic acetylch Drosophila melanog

Alpha 2 subunit of Neuronal nicotinic Prostate cancer-as

Human neuronal nic

Neuronal nicotinic Modified acetylcho Modified hen ACR s Novel human diagno Alpha4 subunit of Alpha4 subunit of Neuronal nicotinic Neuronal nicotinic

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indication or disease associated with aberrant, pathogenic or undestrable antibody production, particularly autoimmune or allergic diseases. The menthod comprises administering a T cell epitope peptide. The sequence of the epitope peptide comprises an immunodominant T cell epitope sequence of the antigen. The antigen comprises the immunodominant T cell epitope sequence. The method can be used to specifically tolerise or down regulate the priming or activity of antigen-specific T cells of a mammal. It can be used to prevent or inhibit an indication or disease associated with antibody production to an antigen specific T cells of a mammal. It can be used to prevent or inhibit an indication or disease associated with antibody production to an antigen such as an endogenous antigen, e.g. acetylcholine receptor, insulh, growth hormone, factor VIII or factor IX, or an exogenous antigen e.g. a fungal antigen, a plant antigen, an antigen of a domestic cat or an antigen of a mite. It can be used to treat autoimmune diseases, as most an antigen of a mite. It can be used to treat autoimmune diseases, as most antigen of a mite. It can be used to treat autoimmune diseases, as most antigen of a mite. It can be used to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, autoimmune haemolytic anaemia, autoimmune thrombocytopaemia, autoimmune astimma, cryoglobulinaemia, thrombic thrombocytopaemia, primary biliary sclerosis, pernicious anaemia or pemphigus. It can be used for treating allergic diseases, e.g. allergic rhinitis, allergic astimma, atopic dermatitis, allergic gastroentheropathy, anaphylaxis, uricaria or angioedema. It can also be used in gene therapy for treating a disease such as haemophilia or diabetes or an indication such as adenosine deamidase deficiency, growth hormone deficiency, insulin sequence represents human acetylcholine receptor which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                  present invention describes a method for preventing or inhibiting an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SEHETRLVAKLEKDYSSVYRPVEDHRQVVEVIVGLQLIQLIUNDEVNQIVTINVRLKQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW
                                                                                                                                                                                       Use of T cell epitope peptides for, e.g. preventing allergies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.7%; Score 1139; DB 21;
Best Local Similarity 99.5%; Pred. No. 2.3e-110;
Matches 209; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Acetylcholine receptor alpha subunit.
                                                                                                                                                                                                                              Example 2; Page 219-221; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                         (MINU ) UNIV MINNESOTA
                                                                                                                                   WPI; 2000-038343/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       457 AA;
                                                                                                                                                      N-PSDB; AAZ38821
                                                                                              Conti-Fine BM;
                       16-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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AAU69151
ID AAU6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptides derived from the hACR-alpha gene product have similar immunogenicity to the gene product, and may be useful in the treatment and diagnosis of myasthenia gravis caused by neuropathy in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFALVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; acetylcholine receptor; AChR; immune response; allergy; antibody-mediated disease; gene replacement therapy; T cell epitope; dermatological; immunosuppressive; antiinflammatory; haemostatic; antianaemic; antiallergic; antiastimatic; antithyroid; antidiabetic; autoimmune disease; allergic disease.
                                                                                                                                                                                                                                                                                                                    New peptide(s) useful in treatment of myasthenia gravis - also in diagnosis, having acetyl:choline receptor-alpha like activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTABLQLIQLINVDEVNQIVTINVRLKQQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1139; DB 6;
Pred. No. 2.3e-110;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human acetylcholine receptor protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRGWKHSVTYSCCPDTPYLDITYHEVMQRL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
407..412
/label= Epitope
/note= "Claim 1 (VII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY56386 standard; Protein; 457 AA.
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1; 13pp; Japanese
                                                                                                                                                                                                                              KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.7%;
99.5%;
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                                                                                                                                                                                       83JP-0186402.
                                                                                                                                                                                                                            (MITU ) MITSUBISHI CHEM IND
                                                                                                                                                    83JP-0186402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune reaction to ACR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.5
Matches 209; Conservative
                                                                                                                                                                                                                                                              WPI; 1985-144120/24.
N-PSDB; AAN50415.
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                                                                           JP60078996-A
                                                                                                                                                    05-OCT-1983;
                                                                                                                                                                                       05-OCT-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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   Active-site
                                                                                                               04-MAY-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                             The invention relates to a composition comprising an isolated acetylcholine receptor (AChR) oligopeptide of about 12 to 20 amino acids. The peptides form a set of 69 overlapping antigenic peptide epitopes which show various affinities for human leukocyte antigens (HLA) HLA-DR2 and DR3. Also included is a composition comprising an antigenic peptide and a Major histocompatibility complex (MHC) component the binding site induces non-responsiveness in a target T cell in a mammal, where the MHC component is an MHC class II component. Peptides with affinity for HLA-DR2 and DR-3 from proteins other than AChR are also included. The composition is used to treat mysathenia gravis and other autoimmune diseases. The present sequence is the human acetylcholine receptor from which the 69 antigenic peptide epitopes are derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
          Human; epitope; autoimmune disease; myasthenia gravis;
Human leukocyte antigen; acetylcholine receptor; HLA DR3; HLA DR2; AChR;
antigen; immunosuppressive; major histocompatibility complex; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                 T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide epitopes of the acetylcholine receptor target helper T cel recognize an antigen in association with an MHC component and are useful to treat autoimmune disease particularly myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTÅGLQLIQLINVDEVNQIVTTNVRLKQQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 437;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1133; DB 22;
Pred. No. 9.1e-110;
0; Mismatches 2;
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                                                                                                                                                                                      Wehner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW83381 standard; Protein; 235
                                                                                                                                                                                                                                                                           Example 1; Fig 1; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.18;
99.08;
                                                                                                                      30-MAR-2001; 2001WO-US10450
                                                                                                                                         31-MAR-2000; 2000US-193745P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208; Conservative
                                                                                                                                                                                      Deshpande S, Spack E,
                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                          WPI; 2001-648547/74
                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AA;
                                                                         WO200174848-A2
                                                     Homo sapiens
                                                                                                11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW83381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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The present sequence represents a human acetylcholine receptor (hAChR) alpha-subunit variant which is used as all or part of a protein for alpha-subunit variant which is used as all or part of a protein for modulating the autoimmune response of an individual to hAChR. The protein can be administered to alleviate and/or treat myasthenia gravis (MG), and is useful for diagnosing the condition. It can be combined with a suitable carrier in pharmaceutical compositions, and is useful for such therapeutic (especially masal or oral) administration and diagnosis. MG is a human neuromuscular disorder, in which autoantibodies against AChR bind to the receptor and interfere with signal transmission comman of the AChR alpha-subunit appears to be the prime target for these autoantibodies, particularly the main immunogenic region (MIR). The protein enables antigen-specific immunotherapy which suppresses only adverse autoimmune responses whilst leaving owerall immune system intext, unlike current methods of treating MG using immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is not given in the specification but has been by the indexer as specified in the claim usin the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 MVDLPRPSCVTLGVPLFSHLQDEQWVDXNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------QWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNN 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poly:peptide(s) modulating auto:immune response to acetyl:choline receptor - comprise all or part of extracellular domain of human acetyl:choline receptor alpha-sub:unit, useful in treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nyasthenia gravis; autoimmune response; neuromuscular disorder;
   variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
acetylcholine receptor alpha-subunit; hAChR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.7e-108;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1111.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Souroujon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Fig -; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                               (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.2%;
88.5%;
                                                                                                                                                                                                                                                                                                                                                                        97IL-0120792.
                                                                                                                                                                                                                                                                                                               98WO-IL00211.
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Best Local Similarity 88.5
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fuchs S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drugs e.g. steroids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV72829
                                                                                                            Homo sapiens
Synthetic.
                                                                                                                                                                                             WO9850544-A1
                                                                                                                                                                                                                                                                                                               06-MAY-1998;
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created by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barchan D,
                                                      diagnosis.
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   Human;
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RESULT 5 AAR06254

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The present sequence represents a human acetylcholine receptor (hAChR) alpha-subunit variant which is used as all or part of a protein for anodulating the autoimmune response of an individual to hAChR. The protein can be administered to alleviate and/or treat myasthenia gravis (MG), and is useful for diagnosing the condition. It can be combined with a suitable carrier in pharmaceutical compositions, and is useful for such therapeutic (especially nasal or oral) administration and diagnosis. MG is a human neuromuscular disorder, in which autoantibodies diagnosis. MG is a human neuromuscular junction. The extracellular from nerve to muscle at the neuromuscular junction. The extracellular domain of the AChR alpha-subunit appears to be the prime target for the protein enables antigen-specific immunotherapy which suppresses only extrace autoantibodies, particularly the main immunotherapy which suppresses only extrace autoimmune responses whilst leaving overall immune system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is not given in the specification but has been by the indexer as specified in the claim usin the sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intact, unlike current methods of treating MG using immunosuppressive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MVDLPRPSCVTLGVPLFSHLQDEQWVDYNLKWNPDDYGGVKKIHIFSEKIWRPDLVLYND 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQ--
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                                                          Human; acetylcholine receptor alpha-subunit; hAChR; variant;
myasthenia gravis; autoimmune response; neuromuscular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAINPESDQPDLSNFMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAINPESDQPDLSNFMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHF 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1088.5; DB 19; Lengtl
Pred. No. 1.7e-105;
1; Mismatches 1; Indels
                  Human acetylcholine receptor alpha-subunit variant 2.
                                                                                                                                                                                                                                                                                                                                                                                                       Souroujon MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 111; Fig -; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis of myasthenia gravis
                                                                                                                                                                                                                                                                                                                                                                (YEDA ) YEDA RES & DEV CO LID.
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88.3%;
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Best Local Similarity 88.3
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Barchan D, Fuchs S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           given in the figures.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-610383/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drugs e.g. steroids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV72830.
                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                  WO9850544-A1.
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                                                                                                                                                                                                                                          12-NOV-1998
                                                                                                                                                               Synthetic.
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                                                                                                 diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTVGLQLIQLINVDEVNQIVTTNVRLKQQW 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptors may be used in assay for materials which modify them. They may be produced in substantial, pure quantities for use in experimentation, development of insecticides without effect on hWNARs and treatment of parasitic infections. MADs raised to the peptides may be useful in detection of the structure of MNARs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human muscle nicotinic acetyl:choline receptor - used to assay
the effects of agents which affect acetyl:choline receptors in
skeletal muscles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 456;
                                                                                                                                                                                            Nicotinic acetyl choline receptor; AchR; TE671; insecticides; Muscle relaxants; anthelmintics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
                                                                                                                                                       Human acetylcholine receptor TE671 (AchR) alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1100.5; DB 1
Pred. No. 2.4e-106;
1; Mismatches 4;
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97.1%;
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                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence reproduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1990-231525/31.
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Best Local Similarity
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                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                             07-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-1988;
                                                                                                                                                                                                                                                                                             CA2003459-A.
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VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptors may be used in assay for materials which modify them. They may be produced in substantial, pure quantities for use in experimentation, development of insecticides without effect on hWNARs and treatment of parasitic infections. Mabs raised to the peptides may be useful in detection of the structure of MNRs. 24 unidentified residues are due to the poor quality of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.0%; Score 1074.5; DB 11; Length 456; Best Local Similarity 93.8%; Pred. No. 1.3e-103; Matches 197; Conservative 6; Mismatches 6; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human muscle nicotinic acetyl:choline receptor - used to assay the effects of agents which affect acetyl:choline receptors in skeletal muscles.
                                                                                      Nicotinic acetyl choline receptor; AchR; TE671; insecticides; Muscle relaxants; anthelmintics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotinic acetyl choline receptor; AchR; TE671; insecticides; Muscle relaxants; anthelmintics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken acetylcholine receptor (AchR) alpha-subunit.
                                                  Mouse acetylcholine receptor (AchR) alpha-subunit.
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                                                                                                                                                                                                                                                                                                                           (SALK ) SALK INST FOR BIOL STUD.
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                                                                                                                                                                                                                                                                                                                                                               Schoepfer RD;
                                                                                                                                                                                                                                                                                         88US-0275422.
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                (first entry)
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                07-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptors may be used in assay for materials which modify them. They may be produced in substantial, pure quantities for use in experimentation, development of insecticides without effect on hWNARs and treatment of parasitic infections. MADs raised to the peptides may be useful in detection of the structure of MNARs. 24 unidentified residues are due to the poor quality of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.1%; Score 1086.5; DB 11; Length 456; 95.7%; Pred. No. 7.1e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human muscle nicotinic acetyl:choline receptor - used to assay
the effects of agents which affect acetyl:choline receptors in
skeletal muscles.
                                                                                                                                                                                                              Nicotinic acetyl choline receptor; AchR; TE671; insecticides; Muscle relaxants; anthelmintics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                          Calf acetylcholine receptor (AchR) alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 7.1e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                   AAR06256 standard; protein; 456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06255 standard; protein; 456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SALK ) SALK INST FOR BIOL STUD
                                                                                                                                                                                                                                                                                                                                                                                                               88US-0275422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schoepfer RD;
                                                                                                                                       07-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 95.7
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1990-231525/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lindstrom JM,
                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                          23-MAY-1990.
                                                                                                                                                                                                                                                                                                        CA2003459-A.
                                                                                                                                                                                                                                                                      Bos taurus.
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27-MAY-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                           62 DYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFALVKFTKVLLQYTGHITWTPP 121
                                                                                                                                                                                                                                                                                                                                                                                                                       122 AIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKES 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acetylcholine receptor; AChR; epitope; myasthenia gravis; human; MHC; mouses, MHC-peptide complex; subunit; antigen; binding site; receptor; T-cell; autoimmune disease; immune system; rheumatoid arthritis; multiple sclerosis; myesthnia gravis.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                       EHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQWV 61
                                                                                                                                                                                                                                                                                                                                                                                21 BHETRLYDDLFREYSKVYRPVENHRDAVVTYGLQLIUVDEVNQIVTTNVRLKQQWV
                                                                                                                                                                                                                                                         hWNARS and treatment of parasitic infections. WADS raised to the peptides may be useful in detection of the structure of MNARS. 22 unidentified residues are due to the poor quality of the
                                                                                                                                                                                                                            Receptors may be used in assay for materials which modify them. They may be produced in substantial, pure quantitles for use in experimentation, development of insecticides without effect on
                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                    Human muscle nicotinic acetyl:choline receptor - used to assay the effects of agents which affect acetyl:choline receptors in
                                                                                                                                                                                                                                                                                                                                DB 11; Length 455;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                              84.8%; Score 969.5; DB 11;
84.2%; Pred. No. 1.2e-92;
ive 16; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acetylcholine receptor protein, alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 ROWKHSVIYSCCPDIPYLDIIYHFLMQRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR36984 standard; Protein; 449 AA.
                                                                                                           (SALK ) SALK INST FOR BIOL STUD.
                                                                                                                            Schoepfer RD;
                                                                   89CA-2003459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.23
Matches 176; Conservative
                                                                                                                                                                                                            Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                          sequence reproduction.
                                                                                                                                                 WPI; 1990-231525/31
                                                                                                                                                                                                                                                                                                            455 AA;
                                                                                                                                                                                        skeletal muscles
                                                                                                                             Lindstrom JM,
                                                                  21-NOV-1989;
                                                                                      23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-SEP-1993
                            CA2003459-A
                                               23-MAY-1990
        Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR36984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182
                                                                                                                                                                                                                                                                                                                                                                                                                               81
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This sequence represents the alpha subunit of acetylcholine receptor protein. This sequence may be used in the construction of an whorepetide complex which comprises an antigenic peptide, eg. AChR where period is anyelin basic protein peptide MBP(1-14)A4, and an isolated MHC subunit component which has an antigen binding site, where the antigenic peptide is associated with the antigen binding site. The MHC-peptide complex selectively binds a T-cell receptor on T-cells associated with diseases, esp. autoimmune diseases. The coding sequence of this protien may be incorporated in to a sequence coding sequence of this protien may be incorporated in to a sequence coding sequence of this protien may be incorporated in the accomplant as the such that, when the subunit is expressed and folded, the AChR peptide antigen will be available as an epitope for the target the immune system which are responsible for undestrable immune responses. They may be used for treating autoimmune disease such as rheumatoid arthritis, multiple sclerosis or myesthnia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 SEHETRIVANILENYNKVIRPVEHHTHFVDITVGLQLIQLISVDEVNQIVETNVRLRQQW 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complexes comprising antigenic peptide and major histocompatibility complex sub-unit - for treatment and diagnosis of immune diseases, e.g. rheumatoid arthritis, multiple sclerosis and myasthenia gravis.
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75.2%; Pred. No. 2e-86;
ive 26; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Sharma SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 YRGWKHWYYYTCCPDTPYLDITYHFIMQRI 222
                   /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR86421 standard; Protein; 449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 3; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Nag B,
                                                                                                                                                                                                                                          92WO-US10031.
                                                                                                                                                                                                                                                                                                   91US-0793938
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                                                                                                                                                                                                                                                                                                                                                                                                                           Clark BR, McConnel HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-182250/22.
                                                                                                                                                                                                                                                                                                                                                               (ANER-) ANERGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ39941
                                                                                                                                                                                                                                          18-NOV-1992;
                                                                                                                                                                                                                                                                                                   19-NOV-1991;
                                                                                                                  WO9309810-A
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Acetyl choline acceptor protein.
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                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                      'note-
                                                                                                                                                                                                                                                                         'note=
                                               Peptides; immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPI; 1984-265833/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461 AA;
                                                                                                                                                                                                                                                                                                                                                                   JP59130254-A
           22-JUL-1992
                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-1983;
                                                                                                                                                                                                                                                                                                                                                                                     26-JUL-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                 Peptide
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                                                                                                                                                                                                                                                                                                                                   The alpha subunit of the electric ray acetylcholine receptor (AChR) (AAR86421) is an autoantigen involved in the pathogenesis of myasthenia gravis. AChR peptide segments, e.g. amino acids 195-215, can be used in the construction of MHC class II-peptide conjugates. Such conjugates are able to inhibit deleterious T-cell mediated immune response, such as allergic reactions, allograft rejection, and autoimmune diseases, or to promote T-cell responses for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                         Acetylcholine receptor; autoantigen; MHC class II; major histocompatibility complex; autoimmunity; autoimmune disease; rheumatoid arthritis; myasthenia gravis; multiple sclerosis;
                                                                                                                                                                                                                                                                             New MHC Class 2-peptide complex for inducing T cell non-responsiveness - opt. including a toxin, esp. for treating auto-immune disease such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 910; DB 17; Length 449; 75.2%; Pred. No. 2e-86; 1. 26; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRGWKHWVYYTCCPDTPYLDITYHFIMORI 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
         Acetylcholine receptor alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP40417 standard; protein; 461 AA
                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6; 47pp; English
                                                                                                                                                                                                                                  SD;
                                                                                                                                              92US-0869293.
88US-0210594.
89US-0367751.
90US-0576084.
                                                                                                                                                                                                                                  Sharma
                                                       allograft rejection; vaccine
                                                                                                                              88US-0210594
                                                                                                                                                                                             91US-0690840
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                  Clark BR, Lerch BL,
                                                                       Torpedo californicus
                                                                                                                                                                                                                (AMER-) AMERGEN INC.
                                                                                                                                                                                                                                                  WPI; 1996-010049/01.
N-PSDB; AAT06284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       449 AA;
                                                                                                                              23-JUN-1988;
                                                                                                                                                                          30-AUG-1990;
28-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Simines 158;
                                                                                                                                                                                             23-APR-1991;
                                                                                         US5468481-A
                                                                                                                                                 14-APR-1992;
                                                                                                                                                          23-JUN-1988
                                                                                                                                                                  21-JUN-1989
                                                                                                            21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
AAP40417
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide(s) - with immuno activity similar to acetyl choline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The polypepides have immunoactivity similar to that of the acetyl choline acceptor. They may be prepd. by solid phase synthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 79.6%; Score 910; DB 5; Length 46 Best Local Similarity 75.2%; Pred. No. 2.1e-86; Matches 158; Conservative 26; Mismatches 26; Indels
                                                              'note= "immunogenic peptide"
                                                                               ..103
hte= "immunogenic peptide"
                                                                                                              95..100
/note= "immunogenic peptide"
                                                                                                                                                                                                                                                     ..196
..e= "immunogenic peptide"
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                                                                                                                                                                     "immunogenic peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                              "immunogenic peptide"
                                   'label= signal_peptide
                                                                                                                                                                                                                                                                                                                   ore
1..256
·∼←e= "immunogenic p
Location/Qualifiers
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/note= "1
                                                                                                                                                                                                                       ..180
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                                                                                                                                                                                     08..113
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(first entry)

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VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                            PAIFKSYCELIVTHFPFDEONCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                         MHC; major histocompatibility complex; toxic conjugate; autoimmunity; autoimmune disease; helper T-cell; T-lymphocyte; acetylcholine receptor; myelin basic protein; I-Ab.
                                                                                                          SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                      193 YRGWKHWVYYTCCPDTPYLDITYHFIMQRI 222
                                                                                                                                                                                                                                                                   Acetylcholine receptor alpha subunit.
                                                                                                                                                                                          AAR45946 standard; Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark BR, Lerch LB,
                                                                                                                                                                                                                                                                                                                                         Torpedo californicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-056406/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ANER-) ANERGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ56918
                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1988;
                                                                                                                                                                                                                                                                                                                                                               US5284935-A.
                                                                                                                                                                                                                                           08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-AUG-1990;
28-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUN-1989;
                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUN-1988
                                                                                                                                                                                                                   AAR45946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Dupont apparatus and technique for rapid multiple peptide synthesis (RAMPS) is used to synthesise the members of a set of overlapping (10 residue overlap), 20 residue peptides form the alpha subunit of Torpedo californus AChR.

The AChR peptide 195-215, which has been characterised as an epitope in mysathenia gravis (MG) in humans and in mice, may be connected to the N-terminal antigen binding site of a polypeptide derived from an MHC antigen associated with MG. For example, if the recombinant complex is to be used in mice, the AChR peptide may be incorporated into a sequence encoding either the I-Ab-alpha or I-Ab-beta chain (see AAQ)5054-55 respectively). If the AChR peptide is to be incorporated into the beta chain, for example, the oligonucleotide may be inserted as a replacement for the leader sequence.
PAIFKSYCEIIVTHFPFDEONCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
            receptor; epitope; myasthenia gravis; MG; antigen; MHC; IAB; alpha; beta; RAMPS; Torpedo californicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pure major MHC-peptide complex - useful in treating deleterious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.0%; Score 903; DB 14; Length 449; 74.8%; Pred. No. 1.1e-85; ive 26; Mismatches 27; Indels
                                                                                                                                                                                                     Alpha subunit of Torpedo californicus AChR (known).
                                              SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                         205 YRGWKHWVYYTCCPDTPYLDITYHFIMQRI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immune response such as auto: immunity
                                                                                                                                                                                                                                                                                                   1..12
/label= sig_peptide
13..449
/label= mat_protein
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                  Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 6; 93pp; English.
                                                                                                                              AAR35057 standard; Protein; 449
                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0690840
                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US03391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 79.0 Best Local Similarity 74.8 Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark BR, Lerch BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-036056/04.
N-PSDB; AAQ35053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ANER-) ANERGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 AA;
                                                                                                                                                                                                                                        binding site;
                                                                                                                                                                                                                              Acetylcholine
                                                                                                                                                                            21-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-APR-1991;
                                                                                                                                                                                                                                                                                                                                                              W09218150-A
                                                                                                                                                                                                                                                                                                                                                                                      29-0CT-1992.
                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                       AAR35057;
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                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                           Protein
121
                                              181
                                                                                                         RESULT 13
                                                                                                                   AAR3505
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5;
                                                                                                                                 The acetylcholine receptor alpha subunit given in sequence AAR45946 (corresponding mRNA in AA056918) and the myelin basic protein given in AAR45947 are antigenic peptides associated with autoantigens. They have been conjugated with MHC class II components such as I-Abalpha chain (encoded by sequence AA056919) or I-Ab-beta chain, encoded by AA056920) and a toxin or label to form conjugates used to target helper I-cells for the treatment of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHI-TWT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
MHC-mediated toxic peptide conjugates - useful for ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.4%; Score 885; DB 15; Length 449; 74.4%; Pred. No. 8.2e-84; Live 26; Mismatches 26; Indels
                                                                                Disclosure; Fig 6.1-6.4; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                               449 AA;
                            auto-immunity
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Gaps

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1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60

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88US-0210594. 89US-0367751. 90US-0576084. 90US-0635840.

88US-0210594

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Search completed: January 14, 2003, 16:53:40 Job time: 142 secs
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                          61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 IDVRLRWNPADYGGIKKIRLPSDDVWLPDLVLYNNADGDFAIVHMTKLLLDYTGKIMMWT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 SEHETRLVANXLENTNKVIRPCEHHTHFVDITYGLQLIGULISVDEVNQIVETNYRLRQQW 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                They may be produced in substantial, pure quantities for use in experimentation, development of insecticides without effect on hWNARS and treatment of parastitic infections. Mabs raised to the peptides may be useful in detection of the structure of MNARS. Unidentified residues are due to the poor quality of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptors may be used in assay for materials which modify them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human muscle nicotinic acetyl:choline receptor · used to assay the effects of agents which affect acetyl:choline receptors in skeletal muscles.
                                                                                                                                                                                                                                                                                             Nicotinic acetyl choline receptor; AchR; TE671; insecticides; Muscle relaxants; anthelmintics;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Indels
                                                                                                                                                                                                                                                                   Fish acetylcholine receptor (AchR) alpha-subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.9%; Score 845; DB 11;
71.9%; Pred. No. 1.3e-79;
11ve 20; Mismatches 39;
                                                                                 ESRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                              181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                AAR06259 standard; protein; 460 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SALK ) SALK INST FOR BIOL STUD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  88US-0275422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lindstrom JM, Schoepfer RD;
                                                                                                                                                                                                                                                                                                                                                                                                                         89CA-2003459
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity /1.9
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence reproduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-231525/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-1988;
                                                                                                                                                                                                                                       07-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                  CA2003459-A.
                                                                                                                                                                                                                                                                                                                                                                                              23-MAY-1990.
                                                                                                                                                                                                                                                                                                                                      Porpedo sp.
                                                                                                                                                                                                          AAR06259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                 180
                                                                                                           192
                                                                                                                                                       RESULT 15
                                                                                                                                                                    AAR06259
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 14, 2003, 16:51:18 ; Search time 49 Seconds (without alignments) 412.005 Million cell updates/sec

US-09-820-339A-2 1143 1 SEHETRLVAKLFKDYSSVVR.....SCCPDTPYLDITYHFVMQRL 210 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues earched:

otal number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID Description	ACHIB1	acetvlchol		nicotinic	nicotinic			acetylchol		nicotinic	nicotinic	nicotinic		acetylchol		nicotinic	9218 nicotinic	nicotinic	1116										
	DB	: :	1 (7	-	7	7	-	a	~	-	7	~	~	7	~	~	~	~	7	~	-	~	~	7	П	~	-	7	7	c
	* Query Match Length	457	445	457	457	457	456	255	461	461	457	457	499	503	495	502	625	627	464	512	622	468	511	452	528	462	267	454	455	7
•	Query Match	40 7		95.9			86.0				77.7			52.0							50.0		49.4						46.6	
	Score	1139	1096	1096	1095	1093	983	915	915	910	888	875	594.5	594.5	588.5	588.5	582.5	577.5	574.5	571.5	571.5	571	564.5		562.5	വ	552	544	532.5	2
	Ø		101	m	4	S	9	7	80	6	10													23	24	25	26	27	28	č

nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	nicotinic acetylch	hypothetical prote	nicotinic acetylch	hypothetical prote	nicotinic acetylch								
A33523	ACFFA2	S16333	138056	T23843	S12359	S12899	ACCHNN	JH0174	ACFFNN	S10505	A55382	A39218	T43634	T25720	ACCH3N
N		7	N	~	C)	~	-	~	-	ď	7	~	~	~	-
464	576	466	423	265	557	200	491	503	521	203	479	470	511	534	416
46.6	45.7	45.5	45.4	45.0	44.4	44.0	41.9	41.9	41.8	41.3	41.1	41.0	40.9	40.6	40.4
532.5	522.5	520.5	518.5	514.5	508	503	479	479	477.5	472	469.5	469	467.5	463.5	461.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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Gaps 9 80

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Indels

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G13872

nicotinic acetylcholine receptor alpha chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Dete: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S13872
R;Mitzemann, V; Stein, E; Barg, B; Konno, T.; Koenen, M.; Kues, W.; Criado, M. Bur. J. Biochem. 194, 437-448, 1990
A;Title: Primary structure and functional expression of the alpha-, beta-, gamma A;Reference number: S13872; MUID:91099317; PMID:1702709
A;Reference number: MNA
A;Molecule type: mRNA
C;Superfamily: acetylcholine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nicotinic acetylcholine receptor alpha chain precursor - mouse C;Species: Mus musculus (house mouse)
C;Date: 24-Jun-1987 #sequence_revision 24-Jun-1987 #text_change 15-Jun-1996
C;Accession: A24383
R;Isenberg, K.E.; Mudd J.; Shah, V.; Merlie, J.P.
Nucleic Acids Res. 14, 5111, 1986
A;Reference number: A24383; MUID:86259081; PMID:3755237
A;Accession: A24383
A;Accession: A24383
                                                                                                                                                                                                                                                                  VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                    1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQOW
                                                                                                                                                                                               PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE
                                                                                                                                                                                                                                                                                                                                                                                     1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;148-162/Disulfide bonds: #status predicted F;161/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query.Match 95.8%; Score 1095; DB 2; Best Local Similarity 94.8%; Pred. No. 5.3e-93; Matches 199; Conservative 6; Mismatches 5;
                                                                            DB 1;
                                                                                                    4.3e-93;
                                                                                                                        3; Mismatches
                                                                         Score 1096;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.9%;
95.2%;
                                                                                               Best Local Similaricy ... Matches 200; Conservative
                                                                            Query Match
                                                                                                                                                                                                                                                                  61
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C; Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 22-Jun-1999
C; Accession: A03169
R; Noda, M.; Furutani, Y.; Takahashi, H.; Toyosato, M.; Tanabe, T.; Shimizu, S.; Kikyotani Nature 305, 818-823, 1983
A; Title: Cloning and sequence analysis of calf cDNA and human genomic DNA encoding alpha A; Reference number: A03168; MUID:84039794; PMID:6688857
                                                                                                                                                                                                                                                                                                                                                   acetylcholine receptor alpha-subunit - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: (0.2-ul-1996 #sequence_revision 02-Jul-1996 #text_change 30-May-1997
C;Accession: 149458
R;Boulter, J; Luyten, W; Evans, K.; Mason, P.; Ballivet, M.; Goldman, D.; Stengelin, S.
Tible: 1solation of a clone coding for the alpha-subunit of a mouse acetylcholine rece
Reference number: 149458; MUID:85292055; PMID:2993547
A;Accession: 149458
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A; Note: four hydrophobic transmembrane segments are found in each of the four kinds of chinds: four hydrophobic transmembrane segments are found in each of the four kinds of c; Comment: The functional receptor molecule has two alpha chains and one each of the bet C; Superfamily: acetylcholine receptor membrane protein; neurotransmitter receptor; F; Reywords: 91ycoprotein; ion channel: membrane protein; neurotransmitter receptor; post F; 1-20/Domain: signal sequence #status predicted <SIG; F; 21-457/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>
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VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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                                                                                                                     1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW
                                                                                             PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M17640; NID:g191601; PID:g191602
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 95.9%; Score 1096; DB 2;
Best Local Similarity 94.8%; Pred. No. 4.2e-93;
Matches 199; Conservative 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-457 <NOD>
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A; Residues: 1-445 <RES>
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Gaps

Indels Length

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nicotinic acetylcholine receptor alpha chain precursor - marbled electric ray (fragme C; Species: Torpedo marmorata (marbled electric ray)
C; Species: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 15-Jun-1996
C; Accession: A93440; A03170
R; Sumikawa, K.; Houghton, M.; Smith, J.C.; Bell, L.; Richards, B.M.; Barnard, E.A.
Nucleic Acids Res. 10, 5809-5822, 1982
A; Title: The molecular cloning and characterisation of cDNA coding for the alpha subu A; Accession: A93440; MUID:83064520; PMID:6183641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain is 40,000.
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
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C;Species: Torpedo marmorata (marbled electric ray)
C;Species: Torpedo marmorata (marbled electric ray)
C;Sacession: 150548
R;Devillers-Thiery, A.; Giraudat, J.; Bentaboulet, M.; Klarsfeld, A.; Changeux, J.P.
Adv. Exp. Med. Biol. 181, 17-29, 1984
A;Title: Molecular genetics of Torpedo marmorata acetylcholine receptor.
A;Reference number: 150548; MUID:85171452; PMID:6549423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-255 <SUM>
C; Comment: The functional receptor molecule has two alpha chains and one each of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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A; Residues: 1-461 <DEV>
A; Cross-references: GB MA2893; NID:q213215; PIDN:AAA96704.1; PID:g213216
C; Superfamily: acetylcholine receptor
C; Keywords: neurotransmitter receptor
                                       AIFKSYCELIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKES
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A;Molecule type: mRNA
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Best Local Similarity 75.73
Matches 159; Conservative
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Matches 159; Conservative
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C. Species: Gallus gallus (chicken)
C. Species: Gallus gallus (chicken)
C. Date: 30-Sep-1991 #seatulore.
C. Date: 30-Sep-1991 #seatulore.
C. Date: 30-Sep-1991 #seatulore.
C. Accession: S00376, A38754; I50148
R. Neff P.; Oneyser C.; Alliod, C.; Couturier, S.; Ballivet, M.
BMB00 J. 7, 595-601, 1988 and the brain define three distinct neuronal nicotinic acetylch A; Receivance number: S00376, WulD:88283624; PMID:3267226
A; Accession: S00376
A; Moccession: S00376
A; Moccession: A38754
A; Coccession: A38754
A; Cocc
A;Residues: 1-457 <ISE>
C;Superfamily: acetylcholine receptor
C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
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                                                                                                             Length 457
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                                                                                                          Score 1093; DB 2; Length 4
Pred. No. 8.2e-93;
7; Mismatches 5; Indels
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84.2%; Pred. No. 1.1e-82;
ive 17: Mismatches 16; Indels
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                                                                                                       Query Match 95.6%;
Best Local Similarity 94.3%;
Matches 198; Conservative
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Matches 176;
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nicotinic acetylcholine receptor alpha chain precursor - African clawed frog C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: J960W-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Accession: A28529
R; Baldwin, T.J.; Yoshihara, C.M.; Blackmer, K.; Kintner, C.R.; Burden, S.J.
J. Cell Biol. 106, 469-478, 1988
A; Title: Regulation of acetylcholine receptor transcript expression during developmen A; Reference number: A28529
A; Molecule type: mRNA
A; Residues: 1-457 < ABAL>
A; Molecule type: mRNA
A; Residues: 1-457 < ABAL>
A; Cross-references: GB:X07067; NID:g64510; PIDN:CAA30103.1; PID:g64511
C; Superfamily: acetylcholine receptor
C; Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra F; 1-20/Domain: signal sequence #status predicted < SIG>
F; 21-457/Product: nicotinic acetylcholine receptor alpha chain #status predicted < AMAT
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C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: S08162
B; Hartman, D.S.; Claudio, T.
Nature 343, 372-375, 1990
A; Title: Coexpression of two distinct muscle acetylcholine receptor alpha-subunits A; Reference number: S08162; MUID:90136925; PMID:2300185
A; Reference number: S08162
A; Molecule type: mRNA
                                                                                                                                                                                                                                          VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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      Length 461;
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                                                              Indels
                                                              26;
DB 1;
79.6%; Score 910; DB 1; 75.2%; Pred. No. 6e-76; ive 26; Mismatches 3
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                                                              Conservative
                            al Similarity
158; Conserv
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                                  Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Torpedo californica (Pacific electric ray)
Date: 30-Apr-1982 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C.Accession: A03170; A20972; A3355; A41587; A54233
R.Noda, M.; Takahashi, H.; Tanabe, T.; Toyosato, M.; Furutani, Y.; Hirose, T.; Asai, M.;
Nature 299, 793-797, 1982
A;Title: Primary structure of alpha-subunit precursor of Torpedo californica acetylcholi A;Accession: A03170
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C.Scomplex: heterotetramer of two alpha chains, one beta chain (see PIR:ACRYB1), one gamm C.Scomplex: heterotetramer of two alpha chains, one beta chain (see PIR:ACRYB1), one gamm C.Scowords: ion channel, membrane protein; neurotransmitter receptor; postsynaptic membr F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-461/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>
F:25-401/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>
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R; Residues: 29-41,82-88,132-149;339-354;363-411 <MOO>

R; COhen, J.B.; Sharp, S.D.; Liu, W.S.

J. Biol. Chem. 266, 23354-23364, 1991

Title: Structure of the agonist-binding site of the nicotinic acetylcholine receptor. Reference number: A41587; MUID: 92078212; PMID:1744130
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124/Domain: signal sequence *status predicted <SIG>
125-461/Product: nicotinic acetylcholine receptor alpha chain *status predicted <MAT>
1236-259/Domain: transmembrane *status predicted <TMI>
1267-285/Domain: transmembrane *status predicted <TMI>
1297-324/Domain: transmembrane *status predicted <TMI>
1297-324/Domain: transmembrane *status predicted <TMI>
1207-324/Domain: transmembrane *status predicted <TMI>
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A; Molecule type: protein
A; Residues: 25-127; 336-421; 429-450 <CON>
A; Residues: 25-127; 336-421; 4.89 driffin, P.R.; Shabanowitz, J.; Martino, P.A.; Hunt,
B; Moore, C.R.; Yates III, J889
Biochemistry 28, 9184-9191, 1989
A; Title: Proteolytic fragments of the nicotinic acetylcholine receptor identified by A; McFerence number: A33555; MUID:90105466; PMID:2605252
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A; Residues: 1-461 <NOD>
A; Cross.references: 0B:J00963; GB:M14810; NID:g213217; PIDN:AAA96705.1; PID:g213218
A; Crost.references: GB:J00963; GB:M14810; NID:g213217; PIDN:AAA96705.1; PID:g213218
B; Conti-Tronconi, B.M.; Hunkapiller, M.W.; Raffery, M.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 2631-2634, 1984
A; Title: Molecular weight and structural nonequivalence of the mature alpha subunits
A; Reference number: A20972; MUID:84194060; PMID:6585820
'A; Accession: A20972
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A; Residues: 104-131 <COH>
A; Note: residue 117-Tyr was shown to be alkylated by [3H]-acetylcholine mustard, an
R; Blanton, M.P.; Cohen, J.B.
Biochemistry 33, 2859-2872, 1994
A; Fitle: Identifying the lipid-protein interface of the Torpedo nicotinic acetylchol
A; Reference number: A54233; MUID:94176477; PMID:8130199
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                                                                                                                                            VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                               PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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                                                                                 84
                                                     SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-50
A;Cross_references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
B;Anand, R.; Lindstrom, J.

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C;Keywords: neurotransmitter receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-495/Product: acetylcholine receptor alpha chain #status predicted <MAT>
                                  nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human c;Species: Homo sapiens (man)
R;Mihovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit o A;Reference number: A33956; MUID:91114756; PMID:1989896
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C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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A. Molecule type: mRNA
A. Residues: 30-503 < ANN>
A. Residues: 80-503 < ANN>
A. Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
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R;Criado, M.; Alamo, L.; Navarro, A.
Neurochem. Res. 17, 281-287, 1992
A;Fille: Primary structure of an agonist binding subunit of A;Reference number: S60589; MUID:92319195; PMID:1620271
A;Accession: S60589
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; Pred. No. 7.7e-47,
41; Mismatches 6
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C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor
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Best Local Similarity 51.0%;
Matches 107; Conservative 41
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A; Residues: 1-495 <CRI>
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nicotinic acetylcholine receptor alpha-3 chain precursor - rat Cispecies: Rattus norregicus (Norway rat)  
C;Species: Rattus norregicus (Norway rat)  
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 08-Nov-1996  
C;Accession: A24572  
R;Boulter, J; Evans, K; Goldman, D; Martin, G; Treco, D.; Heinemann, S.; Patrick, J. Nature 319, 368-374, 1986  
A;Title: Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholine A;Reference number: A24572; MUID:86118671; PMID:3753746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurotransmitter receptor; postsynaptic membrane;
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Keywords: glycoprocein; ion channel; neurotransmitter receptor; posts
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-499/Product: nicotinic acetylcholine receptor alpha chain #status
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                                                                                                                                                                                                                                                                                                                                             Score 875; DB 2;
Pred. No. 9.9e-73;
24; Mismatches 29
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; Pred. No. 7.7e-47;
39; Mismatches 62
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Local Similarity 51.4%;
hes 108; Conservative 3
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157; Conserv
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A; Residues: 1-499 <BOU>
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Throughing acetylcholine receptor alpha-3 chain precursor, neuronal (version 2) - human C; Species: Homo sapiens (man)
C; Species: John 1922 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000
C; Accession: A37040; S24595
R; Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.
Neurosci. Lett. 111, 351-356, 1990
A; Title: Molecular cloning of human neuronal nicotinic receptor alpha-3-subunit.
A; Reference number: A37040
A; Accession: A37040
A; Coss-references: EMBL: X52239; NID: 9177897; PIDN: AAC84176.1; PID: 9177898
A; Cross-references: EMBL: X52239; NID: 9177897; PIDN: AAC84176.1; FID: 9177898
C; Superfamily: acetylcholine receptor; transmembrane protein
F; 1-28/Domain: signal sequence #status predicted <SIG>F; 29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <AMT>
                                    1;
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                                                                                                                                                                                                                                                        PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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                                                                                                                                      22 SDAEHRLFERLFEDYNEIIRPVANVSDPVIIQFEVSMSQLVKVDEVNQIMETNLMLKQIW 81
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                             Indels
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50.5%; Pred. No. 2.8e-46;
tive 40; Mismatches 63;
50.5%; Pred. No. 2.7e-46; ive 41; Mismatches 62;
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Best Local Similarity 50.5%
Matches 106; Conservative
Best Local Similarity 50.59
Matches 106; Conservative
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181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210 209 APGYKHDIKYNCCEEI-YPDITYSLYSRRL 237 ò 셤

Search completed: January 14, 2003, 16:58:18 Job time : 50 secs

121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180

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VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120

1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60 || || || :||:||: || :|| || 29 SEAEHRLFERLFEDYNEITRPVANVSDPVIIHFEVSMSQLVKVDEVNQIMETNLMLKQIW 88

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Gaps

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DB 2; Length 502; Indels

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January 14, 2003, 16:48:33 ; Search time 78 Seconds (without alignments) 111.667 Million cell updates/sec
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1143
1 SEHETRLVAKLFKDYSSVVR.....SCCPDIPYLDITYHFVMQRL 210
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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112892 segs, 41476328 residues Searched:

112892 tal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	homo s	P02709 bos taurus	PO4756 mus musculu	8 rattus	P09479 gallus gall	torpedo	P02710 torpedo cal		Q98880 brachydanio	P22456 xenopus lae	P04757 rattus norv	P32297 homo sapièn	bos ta	P09481 gallus gall	rattus	P43681 homo sapien	homod	Q15822 homo sapien	caras	-	Q15825 homo sapien	P12389 rattus norv	rattus	gallus	gallus	carass	P43143 rattus norv	drosop		Q05901 homo sapien	-	391 rattus	P91766 manduca sex
SUMMARIES	ID	I	ACHA_BOVIN	ACHA_MOUSE	ACHA_RAT	ACHA_CHICK	ACHA_TORMA	ACHA_TORCA	ACH2_XENLA	ACHA_BRARE	ACH1_XENLA	ACH3_RAT	ACH3_HUMAN	ACH3_BOVIN	ACH3_CHICK	ACH4_RAT	ACH4_HUMAN	ACH5_HUMAN	ACH2_HUMAN	ACH3_CARAU	ACH4_CHICK	ACH6_HUMAN	ACH2_RAT	ACH5_RAT	ACH2_CHICK	ACH6_CHICK	ACHO_CARAU	ACH6_RAT	ACH1_DROME	ACH5_CHICK	ACHO_HUMAN	ACHO_CHICK	ACHO_RAT	ACH1_MANSE
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df	Query Match	7.76	95.9	95.9	95.8		80.1				9.92	52.0	52.0	51.5	51.0	50.8	50.5	50.4	50.3	50.0	20.0	49.8	49.4	49.3	49.2	49.0	48.4	48.4	48.3	٠	46.9	٠	46.6	46.5
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P17644 drosophila P18257 carasslus a P23414 schistocerc P25162 drosophila P14144 natrix tess P09484 gallus gall P12390 rattus norv P04755 drosophila Q9ugml homo sapien P17787 homo sapien P43144 rattus norv P26153 gallus gall
ACH2_DROME ACH1_SCHGR ACH1_SCHGR ACH4_DROME ACH3_DROME ACHN_CHICK ACHN_CHICK ACHN_RAT ACH3_DROME ACH9_HUMAN ACH9_RAT ACH9_RAT
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522.5 520.5 508 503 501 479 476.5 472.5 472.5 472.5
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ALIGNMENTS

ACHA_HUMAN STANDARD; PRT; 482 AA. TO PO12708:				•		RP SEQUENCE FROM N.A. (ISOFORM 2). RC TISSUE-Muscle; RX MEDLINE-90291973; PubMed-1694127; RA Beeson D., Morris A., Vincent A., Newsom-Davis J.; RT "The human muscle nicotinic acetylcholine receptor alpha-subunit RT exist as two isoforms: a novel exon."; EMBO J. 9:2101-2106(1990).	RP SEQUENCE FROM N.A. (ISOFORM 1). RC TISSUE—Thymus; RX MEDILINE—95242389; Pubmed=7725386; RA Gattenloehner S., Brabletz T., Schultz A., Marx A., RA Mueller Hermelink HK., Kirchner T.; R. Cloning of a cDNA coding for the acetylcholine receptor RT alpha-subunit from a thymoma associated with myasthenia gravis."; RL Thymus 23:103-113(1994).
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InterPro; IPR000188; GABAA_receptor.
InterPro; IRR001175; Neur_channel.
Pfam; PF02931; Neur_chan_lab; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
PRINTS; PR00253; NETONCHANNEL.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; nonic channel; Glycoprotein; Signal; Alternative splicing; Transmembrane; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
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MISSING (IN ISOFORM 1).
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V -> M (IN SCCMS).
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N -> K (IN SCCMS).
/FTIG=VAR_000284.
T -> I (IN SCCMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> S (IN SCCMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_000285.
S -> I (IN SCCMS)
/FTId=VAR_000286.
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MIM; 601462;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - SUBCELLOLAR LOCATION: Integral membrane protein.
- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 AND 2 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
- I TISSUE SPECIFICITY: 1SOFORM 1 IS DIFFERENTIALLY EXPRESSED ONLY IN THE SKELFTAL MUSCLE, WHEREAS ISOFORM 2 IS CONSTITUTIVELY EXPRESSED IN SKELFTAL MUSCLE, WHEREAS ISOFORM 2 IS CONSTITUTIVELY EXPRESSED IN SKELFTAL MUSCLE, BRAIN, HEART, KIDNEY, LIVER LUNG AND THYMUS.
- I DISEASE: THE ALPHA SUBUNIT IS THE MAIN FOCUS FOR ANTIHODY BINDING IN MYASTHENIA GRAVIS. IS THE ALFARACTERIZED BY SPORADIC MUSCULAR FATIGABILITY AND WEAKNESS, OCCURRING CHIEFLY IN MUSCLES INNERWATED BY CRANIAL NEIVES, AND CHARACTERISTICALLY MUSCLES INNERWATED BY CRANIAL NEIVES, AND CHARACTERISTICALLY CHANNEL CONGENITAL MYASTHERING SYNDROME (SCCMS).
- CHANNEL CONGENITAL MYASTHERIC SYNDROME (SCCMS).
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                                                                                                                                                                                 MEDLINE-95344777; PubMed=7619526;
Sine S.M., Ohno K., Bouzat C., Auerbach A., Milone M., Pruitt J.N. II,
                                                                                                                                                                                                                                                                      "Mutation of the acetylcholine receptor alpha subunit causes a slow-channel myasthenic syndrome by enhancing agonist binding affinity."; Neuron 15:229-239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acetylcholine receptor alpha subunit in patients with the slow-channel congenital myasthenic syndrome."; Hun. MOI. Genet. 6:7767-774(1997).
1- FUNCTION: AFFER BINDIA ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sine S.M.; "New mutations in acetylcholine receptor subunit genes reveal heterogeneity in the slow-channel congenital myasthenic syndrome."; Hum. Mol. Genet. 5:1217-1227(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97026281; PubMed-8872460;
Engel A.G., Ohno K., Milone M., Wang H.-L., Nakano S., Bouzat C.,
Pruitt J.N. II, Hutchinson D.O., Brengman J.M., Bren N., Sleb J.P.,
Talib S., Okarma T.B., Lebkowski J.S.; "Differential expression of human nicotinic acetylcholine receptor alpha subunit variants in muscle and non-muscle tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97301773; PubMed-9158151;
Croxen R., Newland C., Beeson D., Oosterhuis H., Chauplannaz G.,
Vincent A., Newsom-Davis J.;
"Mutations in different functional domains of the human muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS SCCMS SER-198; MET-201; ILE-299 AND ILE-314.
                                                                                           Nucleic Acids Res. 21:233-237(1993).
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EMBL; X02502; CAA26344.1; -.
EMBL; X02503; CAA26344.1; JOINED.
EMBL; X02504; CAA26344.1; JOINED.
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EMBL; X02506; CAA26344.1;
EMBL; X02507; CAA26344.1;
                                                                                                                                                    VARIANT SCCMS SER-198
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(PROBABLE)

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81 MVDLPRPSCVTLGVPLFSHLQNEQWVDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNN 140
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                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                  1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                         156 VAINPESDQPDLSNFMESGEWVIKESRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                     25;
  DB 1; Length 482;
Score 1116.5; DB 1; Length
Pred. No. 3.5e-94;
0; Mismatches 1; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
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S77094; AAD14247.1; X70108; CAA49705.1;

EMBL;

A03168; ACHUAL. S10148; S10148.

EMBL; X02508; CAA26344.1;

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ACHA_MOUSE
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Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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                                            MEDLINE-84039794; PubMed-6688857;
Noda M., Furutani Y., Takahashi H., Toyosato M., Tanabe T.,
Shimizu S., Kikyotani S., Kayano T., Hirose T., Inayama S.,
"Cloning and sequence analysis of faalf cDNA and human genomic DNA
encoding alpha-subunit precursor of muscle acetylcholine receptor.";
Nature 305:818-823(1983).
-i- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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                                                                                                                                                                                                              SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA CHAIN.
                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSOCIATED WITH RECEPTOR ACTIVATION.
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Pred. No. 2.4e-92;
3; Mismatches 7; Indels C
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InterPro; IPR001189; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Fam; PF02931; Neur_chan_LBD; 1.
Ffam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGR00860; LIC; 1.
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Best Local Similarity 95.2%;
Matches 200; Conservative 3
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457
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457 AA;
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NCBI_TaxID=9913;
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212
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 13-457 FROM N.A.

MEDLINE-85292055; PubMed-2993547;

MEDLINE-WILL JUYTEN W., Evans K., Mason P., Ballivet M., Goldman D.J.,

Stengelin S.F., Martin G., Heinemann S.F., Patrick J.;

Stengelin S.F., Martin G., Heinemann S.F., Patrick J.;

"Isolation of a clone coding for the alpha-subunit of a mouse acetylcholine receptor";

J. Neurosci. 5:2545-2552(1985).

-I-FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-86559081; PubMed-3755237;
Isenberg K.E., Mudd J., Shah V., Merlie J.P.;
Inuclectide sequence of the mouse muscle nicotinic acetylcholine receptor alpha subunit.";
Nucleic Acids Res. 14:5111-5111(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLUIAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE 1 DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                              13-AUG-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
 457 AA.
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MGD; MGI87885; Chrnal.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
 PRT;
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Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
               13-AUG-1987 (Rel. 05, Created)
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457
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281
316
428
447
162
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=10090;
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                                                                                                  CHRNA1 OR ACRA.
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Transmembrane
ACHA_MOUSE
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                                                                                                                                     ö
                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFALVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                            PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  From rat muscle.";
Fur. J. Biochem. 194:437-448(1990).
Fur. J. Biochem. 194:437-448(1990).
Fur. J. Function: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91099317; PubMed-1702709; Witzemann V., Stein E., Barg B., Konno T., Koenen M., Kues W., Ciddo M., Hofmann M., Sakmann B., Parimary structure and functional expression of the alpha-, beta-, gamma-, delta- and epsilon-subunits of the acetylcholine receptor
ASSOCIATED WITH RECEPTOR ACTIVATION.
N-LINKED (GICNAC. . ) (PROBABLE).
C -> S (IN REF. 2 AND 3).
5CB606D144F29436 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE LICAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE F
DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
MUSCLE) CHAINS.
                                                                                                                                     ö
                                                                                               Length 457;
                                                                                                                                   5; Indels
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15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
                                                                                           95.9%; Score 1096; DB 1; 94.8%; Pred. No. 2.4e-92;
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                                                                                                                                   6; Mismatches
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InterPro; IPR000188; GABAA_receptor.
InterPro: IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
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51938 MW;
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                                                                                                                                   Conservative
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                                                       457 AA;
                                                                                                               Similarity
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TIGRPAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFALVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87144271; PubMed-3821734;
Klarsfeld A., Daubas P., Bourachot B., Changeux J.-P.;
Harsfeld A., Daubas P., Hourachot B., Changeux J.-P.;
Ha S'-flanking region of the chicken acetylcholine receptor alphasubunit gene confers tissue specificity and developmental control of
                                                                                                                                                                                                                                                                                                 Gaps
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                                                                BY SIMILARITY.
ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
CHAIN.
                                                                                                                                              POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
BY SIMILARITY.
ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                  95.8%; Score 1095; DB 1; Length 457; 94.8%; Pred. No. 3e-92; ive 6; Mismatches 5; Indels (
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Nef P., Oneyser C., Alliod C., Couturier S., Ballivet M.;
"Genes expressed in the brain define three distinct neuronal
nicotinic acetylobline receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-7001/2002 (Rel. 41, Last annotation update)
Acctylcholine receptor protein, alpha chain precursor.
Gallus gallus (Chicken).
                                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (P. 776AE3BBDF8F68F3 CRC64;
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SEQUENCE OF 180-227 AND 260-333 FF
MEDLINE-84206570; PubMed-6327170;
 NRIONCHANNEL.
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51866 MW;
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SEQUENCE OF 1-12 FROM N.A.
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457 AA;
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MEDLINE-85270494; PubMed-3860855; Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,

Ballivet M., Nef P., Stalder R., Fulpius B.; "Genomic sequences encoding the alpha-subunit of acetylcholine

Cold Spring Harb. Symp. Quant. Biol. 48:83-87(1983).

SEQUENCE OF 21-44.

are conserved in evolution.

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                                                                                                                 Ray N., Raftery M.A.;
"Brain and muscle nicotinic acetylcholine receptors are different but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00236; NEUROFR TON CHANNEL; 1. Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                              homologous proteins.";
Proc. Natl. Acad. Sci. U.S.A. B2:5208-5212(1985).
-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                       SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELTA, AND GAMAA CHAINS.
SUBCELLULAR: LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
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X12434; CAA30282.1; JOINED.
X124435; CAA30282.1; JOINED.
X12435; CAA30282.1; JOINED.
X07335; CAA30282.1; JOINED.
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PIR; A25738; A25738.
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ASSOCIATED WITH RECEPTOR ACTIVATION, -LINKED (GLCNAC. .) (PROBABLE). -> D (IN REF. 4). 0B31B6EABD7B4D42 CRC64; Length 456; 86.0%; Score 983; DB 1; Length 45: 84.2%; Pred. No. 4.7e-82; uismatches 16; Indels N-LINKED (E -> D (TN 52183 MW; 161 212 160 33 456 AA; DISULFID CARBOHYD CONFLICT SEQUENCE Query Match

RECEPTOR PROTEIN, ALPHA

EHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQWV 61

Conservative

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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
Torpedo marmorata (Marbled electric ray).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                                                                                                                                                                                                           "The molecular cloning and characterisation of cDNA coding for the alpha subunit of the acetylcholine receptor."; Nucleic Acids Res. 10:5809-5822(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-83169822; PubMed-6572962;
Devillers-Thiery A., Giraudat J., Bentaboulet M., Changeux J.-P.;
"Complete mRNA coding sequence of the acetylcholine binding alphasubunit of Torpedo marmorata acetylcholine receptor: a model for thransmembrane organization of the polypeptide chain.";
Proc. Natl. Acad. Sci. U.S.A. 80:2067-2071(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular genetics of Torpedo marmorata acetylcholine receptor."; Adv. Exp. Med. Biol. 181:17-29(1984).
DYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTPP
                                                 AIFKSYCELIVIHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-85171452; PubMed-6549423;
Devillers-Thiery A., Giraudat J., Bentaboulet M., Klarsfeld A.,
                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-335 AND 341-411 FROM N.A.
MEDLINE-83064520; PubMed-6183641;
Sumikawa K., Houghton M., Smith J.C., Bell L., Richards B.M.,
                                                                                                                                                                                         461 AA
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between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ This SWISS-PROT entry is copyright. It is produced through a collaboration -i- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELTA, AND GAMMA CHAINS.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY. MEMBRANE.

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DISULFIDE BONDS.
MEDLINE-86250692; PubMed-3722144;
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Matches 158; Conservative
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PDB; 1ABT; 31-JAN-94.
PDB; 1TOR; 08-MAR-96.
PDB; 1TOS; 08-MAR-96.
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Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
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MEDILINE-8303043; PubMed-6182472;
MEDILINE-8303043; PubMed-6182472;
MOda M., Takahashi H., Tanabe T., Toyosato M., Furutani Y.,
Hirose T., Asal M., Inayama S., Miyata T., Numa S.;
"Primary structure of alpha-subunit precursor of Torpedo californica accetylcholine receptor deduced from cDNA sequence.";
Nature 299:793-797(1982).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
Torpedo californica (Pacific electric ray).
Bukaryota, Metazoa; Chordata, Cranidata, Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristioralea; Batoidea;
Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
                                                                                                                                                                                                     ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
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- L (IN REF. 3).
-> C (IN REF. 3).
5354B3FB451D4F8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              80.1%; Score 915; DB 1; Length 461; 75.7%; Pred. No. 7.3e-76; ive 25; Mismatches 26; Indels
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or send an email to license@isb-sib.ch).
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                                                          PIR; A93440; A93440.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfan; PF02931; Neur_chan_LBD; 1.
Pfan; PF02932; Neur_chan_memb; 1.
                         EMBL; J00963; -; NOT_ANNOTATED_CDS.
                                                                                                                         PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                       52794 MW;
                                                  EMBL; M14807; AAA49273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 159; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7787;
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235
267
301
3321
3321
152
216
216
347
448
                                                                                                                                                                             Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACHA_TORCA
P02710;
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TRANSMEM
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DISULFID
DISULFID
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACHA_TORCA
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GlycosuitedB; P02710; -.

InterPro; IPR000188; GABAA_receptor.

InterPro; IPR001175; Neur_channel.

Pfam; PF02931; Neur_chan_memb; 1.

PRINTS; PR00522; NRIONCHANNEL.

TIGRFAMS; TIGRO0860; LIC; 1.

PROSITE; PS00236; NEUROFR, ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Kao P.N., Karlin A.;
"Acetylcholine receptor binding site contains a disulfide cross-link
                                                                                                                                                                                                                                                                                                                                   -1- SUBUNTT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELTA, AND GAMMA CHAINS.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                              Basus V.J., Song G., Hawrot E.;
"NMR solution structure of an alpha-bungarotoxin/nicotinic receptor
peptide complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSOCIATED WITH RECEPTOR ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 461;
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52740 MW; 398C86C9309AF0D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.6%; Score 910; DB 1; Le
75.2%; Pred. No. 2.1e-75;
ive 26; Mismatches 26;
                                                       between adjacent half-cystinyl residues.";
J. Biol. Chem. 261:8085-8088(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                                                                          MEDLINE-94059936; PubMed-8241115;
                                                                                                                                                                                                                                                                 Biochemistry 32:12290-12298(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00963; AAA96705.1; -.
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                                                                                                         121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                     Baldwin T.J., Yoshihara C.M., Blackmer K., Kintner C.R., Burden S.J.; "Regulation of acetylcholine receptor transcript expression during development in Xenopus laevis.";
                                                         61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                   144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-1B
                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell Biol. 106:469-478(1988).
FUNCTION: AFFER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
                      SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW
                                                                                                                                                                                                                                                                                   01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-1B chain precursor.
Xenopus laevis (African clawed frog).
Bustrychai Metazoa; Chordatu; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUSCLE) CHAINS.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE I DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Postsynaptic membrane; Ionic channel; Glycoprotein; Signal; Transmembrane.
                                                                                                                                                                                                                                                457 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                           SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                      205 YRGWKHWVYYTCCPDTPYLDITYHFIMQRI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A28529; A28529.
InterPro: IPR000188; GABAA_receptor.
InterPro: IPR001195; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NEURORANNEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Muscle;
MEDLINE=88115597; PubMed=3339098;
                                                                                                                                                                                                                                                                       01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X07067; CAA30103.1; -.
                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUSCLE) CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-8355;
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P05377;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes,
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
                                                                                                                                                                                                                                                                                                    21 TDHETRLIGDLFANYNKVVRPVETYKDQVVTVGLQLIQLINVDEVNQIVSTNIRLKQQW
                                                                                                                                                                                                                                                                            1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                            ASSOCIATED WITH RECEPTOR ACTIVATION.
                                                                                                                                  (PROBABLE)
                                                                                                                                                                                            Length 457;
                                                                                                                                                                                   77.7%; Score 888; DB 1; Length 45
75.2%; Pred. No. 2.1e-73;
1vp 23: Mismatches 29; Indels
                                                                                                                               N-LINKED (GLCNAC. . .) (P) 202A84A150C4DB11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha chain precursor.
                                                                                                                                                                                                                ; Pred. No. 2.1e
23; Mismatches
                                               CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 YRCWKHWVYYTCCPDKPYLDITYHFVLQRL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U70438; AAB16917.1; -.
ZFIN; ZDB-GENE-980526-137; chrnal.
InterPro; IPR000188; GABAA_receptor.
                                                                                                                                                   Ψ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U70436; AAB09701.1; -. EMBL; U70437; AAB09770.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DELTA, AND GAMMA CHAINS
281
316
428
447
162
213
161
52107 M
                                                                                                                                                                                                                  Best Local Similarity 75.2
Matches 158; Conservative
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    263
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457 AA;
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Q98880;
                                                                                    DISULFID
      TRANSMEM
TRANSMEM
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                                                                     TRANSMEM
                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACHA_BRARE
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TISSUE SPECIFICITY: OOCYTES. SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                 SIGNAL
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                                                                                                                                                                                                                                                           CHAIN
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InterPro; IPR001175; Neur_channel.
Pfam; PF02331; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGRRAMS; TIGR00860; LIC; 1.
PROSTIE; PS00236; NEUROYR_ION, CHANNEL; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                            61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFALVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                        121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                              1 SEDETRLVKTLFTGYNKVVRPVSHFKDPVVVTVGLQLIQLISVDEVNQIVTSNVRLKQQW 80
                                                                                                                                                                                                                                                                                                  1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA, DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
                                                                                                  ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hartman D.S., Claudio T.; "Coexpression of two distinct muscle acetylcholine receptor alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylcholine receptor protein, alpha-1A chain precursor.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                 ASSOCIATED WITH RECEPTOR ACTIVATION (BY SIMILARITY).
                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL) 336825C5E35BC6F3 CRC64;
                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                       Length 456;
                                                                                                                                                                                                                                                                              29; Indels
                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                       Score 882; DB 1;
Pred. No. 7.3e-73;
22; Mismatches 29
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                                                                                                                                                                                        SIMILARITY.
                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457
                                                                                                                                                                                                                                                                                                                                                                                                                                181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                             201 YRSWKHWVYYACCPDTPYLDITYHFLLLRL 230
                                                                                                                                             POTENTIAL.
                                                                                                                                  POTENTIAL.
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                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Muscle;
MEDLINE=90136925; PubMed=2300185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s during development."; 343:372-375(1990).
                                                                                                                                                                                                                                  52100 MW;
                                                                                                                                                                                                                                                       77.28;
75.78;
                                                                                                                                                                                                                                                                             159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                       20
456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                                                                  456 AA;
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                       161
                                                                            ransmembrane.
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P22456;
                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
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Nature 34
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SEDESRLINDLFKSYNKVVRPVKAFKDKVVVTVGLQLIQLINVNEVNQIVTTNVRLKQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
CHRNA3 OR ACRA3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSOCIATED WITH RECEPTOR ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROBABLE)
                                                                                                                                                                                                        PIR; S08162; S08162.
InterPro; IRR000188; GARA_receptor.
InterPro; IRR000188; GARA_receptor.
InterPro; IRR001175; Neur_channel.
Pfam; PF02931; Neur_chan_memb; 1.
Pfam; FF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCRANNEL.
PROSITE; PS00236; NEUROFR_ION_CHANNEL; 1.
PROSITE; PS00236; NEUROFR_ION_CHANNEL; 1.
POSTSYNAPLIC membrane; Ionic channel; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 457;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (PI
8728D227D905ED10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.6%; Score 875; DB 1;
74.8%; Pred. No. 3.2e-72;
ive 24; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL
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MEDLINE-86118671; PubMed-3753746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM;
                                                                                                                                                                                       EMBL; X17244; CAA35109.1; -.
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457
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428
447
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213
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212
161
457 AA;
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TRANSMEM
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P04757;
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096632 heliothis v

068753 mes musculu

046134 locusta mig

046134 locusta mig

046138 heliothis v

084751 drosophila

09072 drosophila

09072 drosophila

09072 drosophila

09073 drosophila

09187 caenorhabdi

09090 caenorhabdi

090187 caenorhabdi

09018 drosophila

09673 drosophila

09673 drosophila

098776 drosophila
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A Straubberg R.;
Straubberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
C: 1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
DR EMBL; BCO06314; AAH06314.1; -..
R interPro; IPR001175; Neur_channel.
DR Fiam; PF02931; Neur_channel.
PROMITE; PR02932; Neur_channel.
PROMITE; PR02932; Neur_channel.
PRINTS; PR0252; NRIONCHANNEL.
DR PRINTS; PR00236; NEUROTR_ION_CHANNEL; 1.
MINITARIAR PROFICE (MANDEL).
TRANSMEMBLANDEL.
TRAN
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08t0y9 aplysia cal
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to cholinergic receptor, nicotinic, alpha polypeptide 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             269 AA; 30769 MW; 1874BFB614CEF18F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
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Q9PTS8
Q8T7S0
                                        096632
Q8R5H3
Q46133
O46134
Q46128
Q8WRS1
Q9WRS1
                                                                                                                                                                                        Q9U940
Q8T7S3
Q9VC72
Q8T7R9
Q9C8U9
Q9C6132
Q8T7S1
Q9T7S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8T7V5
Q9VC74
Q9VWI8
Q9XZI3
Q8SXP7
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Homo sapiens (Human).
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Best Local Simi
Matches 209; (
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Q9BRE6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9bre6 homo sapien
Q9xs62 canis famil
                                                                                                                                         ; Search time 112 Seconds
(without alignments)
386.338 Million cell updates/sec
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                                                                                                                                                                                                                                                                             210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                          1 SEHETRLVAKLFKDYSSVVR.....SCCPDTPYLDITYHFVMQRL
                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                           tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
                                                                                                                                            January 14, 2003, 16:49:47
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Q8VHH6
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Q923N8
Q923N7
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P91764
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Q8SPU7
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                                                                                                                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
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2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
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sp_rodent:*
sp_virus:*
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length: 2000000000
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Match Length
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61 VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                "Expression of mouse nicotinic acetylcholine receptor genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SEHETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to cholinergic receptor, nicotinic, alpha polypeptide 3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 11; Length 341;
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Nicotinic acetylcholine receptor alpha 3 subunit (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 52.0%; Score 594.5; DB 11; Length Best Local Similarity 51.4%; Pred. No. 1.7e-46; Matches 108; Conservative 39; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                               developing thymus.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FB8325B5DB07E139 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 APGYKHEIKYNCCEEI-YQDITYSLYIRRL 234
                                                                                                                                                                                                                                                                                                                                             EMBL. AF32346; AAL37362.1;
InterPro: IPR001189; GABAA_receptor.
InterPro: IPR001175; Neur_channel.
Pfam. PF02931; Neur_chan_EBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PFNTS; PF02925; NEUROHANDEL.
TIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341
39386 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                          STRAIN-C57BL/6;
Kuo Y.-P., Lukas R.J.;
                                                                          musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshioka T., Uzuka Y., Tanabe S., Sarashina T., Ishiguro N.; "Molecular cloning of the canine nicotinic acetylcholine receptor alpha-subunit gene and development of the ELISA method to diagnose
                         PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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Pred. No. 2.4e-92;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Nicotinic acetylcholine recepter alpha-subunit.
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                                                                                                                                                                                                   SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
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                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=MUSCLE;
MEDLINE=20092256; PubMed=10628675;
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95.2%;
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                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myasthenia gravis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9615
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Q9XS62;
61
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VDYNLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. SYALANDARAL GLAND; SATAIN-DBA/21BG; SILIZEL J.A.; Stitzel J.A.; Cautner M.A., Stitzel J.A.; "Cloning of mouse nicotinic acetylcholine receptor alpha 3 subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 SEAEHRLFQYLFEDYNEIIRPVANVSHPVIIQFEVSMSQLVKVDEVNQIMETNLWLKQIW
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UDN-2002 (TrEMBLrel. 21, Last annotation update)
BM401L17.2.1 (cholinergic receptor, nicotinic, alpha polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.0%; Score 594.5; DB 11; Length 51.4%; Pred. No. 2.8e-46; ive 39; Mismatches 62; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL450341; CAC40724.1; '.
InterPro; IPR000188; GABAA_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AF472588; AAL84757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 AA; 57109 MW; 721650E3F38D00FD CRC64;
                                                                                                                                                                                                                                                    QBR4G9 PRELIMINARY; PRT; 499 AA.
QBR4G9;
QB-1JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Nicotinic acetylcholine receptor alpha 3 subunit.
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                                                                                                                 PRT;
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Matches 108; Conservative
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01-DEC-2001 (
01-DEC-2001 (
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PAIFKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKE 180
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                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.0%; Score 594.5; DB 11; Length 499; 51.4%; Pred. No. 2.8e-46;
                                                                       Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                              DB 4; Length 489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TRAIN-CSTBL/GJ; TISSUE-BRAIN;
Brill J., Becker K., Becker C.-M.;
"Mouse neuronal nicotinic acetyl choline receptor alpha 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last annotation update)
Neuronal nicotinic acetylcholine receptor alpha 3 subunit.
                                                                                                                                                          52.0%; Score 594.5; DB 4; Length 51.0%; Pred. No. 2.7e-46; ive 41; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF45029, AAL58471.1; -
InterPro; IPR000145; CytC_hem__bind.
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001189; GABAA_receptor.
InterPro; IPR001175; Neur_chan_EBD; 1.
Pfam; PF02931; Neur_chan_EBD; 1.
PRO351; Neur_chan_memb; 1.
PRINTS; PR00252; NRIONCHANNEL.
TIGREAMS; TIGRONGHANNEL.
PROSETTER: DATA CONTROLLED TO THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           499 AA; 57125 MW; D21650F6A6D7C14B CRC64;
                                                                                                               489 AA; 55636 MW; F8C4F79BDC30A44E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 2.8e-46; 39; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 AA.
TIGRPAMS; TIGRO0860; LIC; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : |:|| : |:|| : | |||| ::|| APGYKHDIKYNCCEEI-YPDITYSLYIRRL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 SRGWKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                       Transmembrane
                                                                                                                                                                                                         107;
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                                                                                                               SEQUENCE
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor
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                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152
                                                                                                                                                                                                         Matches
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Q8VHH6
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Gaps 9

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-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
EMBL; AF225912; AAF34716.2; -.
MGD; MGI:87888; Chrna4.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Stitzel J.A., Jimenez M., Smolen A., Modir J.; "Cloning of mouse nicotinic acetylcholine receptor subunit alpha 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Neuronal nicotinic acetylcholine receptor alpha5 subunit.
Bos taurus (Bovine).
Eukaryota: Metacoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQWVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 NLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTPPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 FKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKESRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.3%; Score 575.5; DB 11; Length Best Local Similarity 52.7%; Pred. No. 2.1e-44; Matches 109; Conservative 33; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    629 AA; 70319 MW; 78C28EDFE371FB2F CRC64;
                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Nicotinic acetlycholine receptor alpha 4 subunit.
CHRNA4 OR ACRA4.
                                                                                                                                                     629 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1
      184 WKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
PRINTS; PR00252; NRIOWCHANNEL.
IIGRFAMS; IIGR00860; LIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 WKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                     PRT;
                                    TYNTRKYECCAEI-YPDITYAFIIRRL
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-LONG SLEEP SELECTED LINE;
                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
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                                             219
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                                                                                                                                                                                                                                                                                                                                                            64 NLKWNPDDYGGVKKIHIPSEKIWRPDLVLYNNADGDFAIVKFTKVLLQYTGHITWTPPAI 123
                                                                                                                                                                                                                                                                                                                                                                                                                       124 FKSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINPESDQPDLSNFMESGEWVIKESRG 183
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ETRLVAKLFKDYSSVVRPVEDHRQVVEVTAGLQLIQLINVDEVNQIVTTNVRLKQQWVDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last senotation update)
01-UN-2002 (TremBLrel. 21, Last annotation update)
8M4011.17.2.2 (cholinergic receptor, nicotinic, alpha polypeptide 4 (isoform 2)).
                                                                                                                                                                  50.8%; Score 580.5; DB 11; Length 629; 53.1%; Pred. No. 7.2e-45; ive 32; Mismatches 64; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.8%; Score 580.5; DB 11; Length 53.1%; Pred. No. 7.3e-45; ative 32; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL; A4450341; CAC40425.1; -...
InterPro; IPR000188; GABAA_receptor.
InterPro; IPR001175; Neur_channel.
Pfam; PF02931; Neur_chan_EBD; 1.
Pfam; PF02931; Neur_chan_memb; 1.
IIGRFAMS; TIGR00860; LIC; 1.
                                                                                                                             629 AA; 70304 MW; 261455B6ED50B41C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641 AA; 71747 MW; BEEBFF1164C1C4AO CRC64;
                                                                TIGRFAMS; TIGRO0860; LIC; 1.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00236; NEUROTR_ION_CHANNEL; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 WKHSVTYSCCPDTPYLDITYHFVMQRL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: | || : | || || 219 TYNTRKYECCAEI-YPDITYAFIIREL 244
InterPro; IPR001175; Neur_channel.
Pfam; FF02931; Neur_chan_LBD; 1.
Pfam; PF02932; Neur_chan_memb; 1.
TIGREAMS; TIGREO0860; LIC; 1.
                                                                                                                                                                  Query Match
Best Local Similarity 53.1%
Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 110; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                             SEQUENCE
                                                                                                          Receptor
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